

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:24:46 ; Search time 21 Seconds
(without alignments)
59.547 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1827

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.5	46.5	12	2	PT0216
2	30	41.7	12	2	S47394
3	29.5	41.0	13	2	S47357
4	29	40.3	12	2	S25549
5	28	38.9	12	2	PH1463
6	28	38.9	12	2	PH1466
7	28	38.9	13	2	S47400
8	27	37.5	11	2	PT0217
9	27	37.5	12	2	S47391
10	27	37.5	13	2	S47383
11	26	36.1	11	2	S57575
12	26	36.1	12	2	S47395
13	26	36.1	13	2	S47381
14	25.5	35.4	13	2	S47382
15	25	34.7	10	2	S23371
16	25	34.7	11	2	PH0947
17	25	34.7	12	2	PH1469
18	25	34.7	12	2	PH1457
19	24.5	34.0	12	2	PH1457
20	24	33.3	11	2	PH1583
21	24	33.3	12	2	S26552
22	24	33.3	12	2	S26559
23	24	33.3	12	2	S26554
24	24	33.3	12	2	S47363
25	24	33.3	12	2	PH1467
26	24	33.3	12	2	PH1468
27	24	33.3	13	2	S47390
28	23.5	32.6	12	2	PH1459
29	23.5	32.6	13	2	S47377

30 23 31.9 12 2 S26557 T-cell receptor be
31 23 31.9 12 2 S26556 T-cell receptor be
32 23 31.9 12 2 S26553 T-cell receptor be
33 23 31.9 12 2 PH1462 T-cell receptor be
34 23 31.9 12 2 PH1470 T-cell receptor be
35 23 31.9 12 2 PH1464 T-cell receptor be
36 23 31.9 13 2 A23695 myosin heavy chain
37 22.5 31.2 12 2 S26541 T-cell receptor be
38 22.5 31.2 12 2 PH1458 T-cell receptor be
39 22.5 31.2 13 2 S47356 T-cell antigen rec
40 22.5 31.2 13 2 S47378 T-cell antigen rec
41 22.5 31.2 13 2 S47385 T-cell antigen rec
42 22 30.6 10 2 PH0927 T-cell receptor be
43 22 30.6 12 2 S26546 T-cell receptor be
44 22 30.6 12 2 S26547 T-cell receptor be
45 22 30.6 12 2 S26555 T-cell receptor be

ALIGNMENTS

RESULT 1

PT0216 T-cell receptor beta chain V-J region (4-1-G.4) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C:Accession: PT0216
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict

A:Reference number: PT0209; MUID:91217621; PMID:1902501

A:Accession: PT0216

A:Molecule type: mRNA

A:Residues: 1-12 <NAK>

C:Keywords: T-cell receptor

Query Match 46.5%; Score 33.5; DB 2; Length 12;

Best Local Similarity 72.7%; Pred. No. 12;

Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11

DB 1 CASSLIG-TTNT 10

RESULT 2

S47394

T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47394; S47369

R:Rehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A:Reference number: S47355

A:Accession: S47394

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-12 <LEH>

A:Cross-references: EMBL:Z35714; NID:9527523; PIDN:CAA84783.1; PID:9527524; EMBL:Z35694;

Query Match 41.7%; Score 30; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 51;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 12

DB 1 CASSIGNGYTTF 12

RESULT 3

S47357

```
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47357
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell
A:Reference number: S47355
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35681; NID:G527451; PIDN:CAA84750.1; PID:G527452
C:Keywords: T-cell receptor

Query Match 41.0%; Score 29.5; DB 2; Length 13;
Best Local Similarity 63.6%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
   ||| :|||
Db 1 CASS-GRSTDT 10
   ||| :|||

RESULT 4
S26549
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26549; S26550
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26549
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X67999
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
A:Accession: S26550
A:Molecule type: mRNA
A:Residues: 1-12 <CA2>
A:Cross-references: EMBL:X68000
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 40.3%; Score 29; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 77;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGKS 8
   ||| :|||
Db 1 CASSLGST 8
   ||| :|||

RESULT 5
PH1463
T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1463
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1463
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell
```

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Query Match 38.9%; Score 28; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKS 8
   ||| :|||
Db 1 CASSLGNT 8
   ||| :|||

RESULT 6
PH1466
T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1466
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1466
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 38.9%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7
   ||| :|||
Db 1 CASSLGQ 7
   ||| :|||

RESULT 7
S47400
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47400
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47400
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35678; NID:G527535; PIDN:CAA84747.1; PID:G527536
C:Keywords: T-cell receptor

Query Match 38.9%; Score 28; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
   ||| :|||
Db 1 CASSVALATEAF 12
   ||| :|||

RESULT 8
PT0217
T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0217
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restri
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0217
A:Molecule type: mRNA
```

A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELKG 6
||| ||
Db 1 CASRLG 6

RESULT 9

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47391; S47386

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A;Reference number: S47355

A;Accession: S47391

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-12 <LEH>

A;Cross-references: EMBL:Z35712; NID:G527519; PIDN:CAA84781.1; PID:G527520; EMBL:Z35701;
C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELKGKSTNTF 12
||| | ||
Db 1 CASSTGSYGTYF 12

RESULT 10

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47383

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A;Reference number: S47355

A;Accession: S47383

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>

A;Cross-references: EMBL:Z35709; NID:G527513; PIDN:CAA84778.1; PID:G527514
C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELKGKS 8
||| : ||
Db 1 CASSMGGS 8

RESULT 11

T cell receptor V-J junctional alpha chain region - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57575

R;Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argat, V.P.

submitted to the EMBL Data Library, June 1995

A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b

A;Reference number: S57494

A;Accession: S57575

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <BUR>

A;Cross-references: EMBL:Z49953; NID:G887510; PIDN:CAA90224.1; PID:G887511
C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELKG 7
||| : ||
Db 1 CASQGGK 7

RESULT 12

S47395

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C;Accession: S47395

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A;Reference number: S47355

A;Accession: S47395

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-12 <LEH>

A;Cross-references: EMBL:Z35715; NID:G527525; PIDN:CAA84784.1; PID:G527526
C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELKGKSTNTF 12
||| | ||
Db 1 CASSQGSYGTYF 12

RESULT 13

S47381

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C;Accession: S47381

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A;Reference number: S47355

A;Accession: S47381

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>

A;Cross-references: EMBL:Z35698; NID:G527487; PIDN:CAA84767.1; PID:G527488
C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELKGKSTNTF 12
||| : ||
Db 1 CASSTRSNTFAP 12

RESULT 14

S47382

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47382; S47370
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A;Reference number: S47355
A;Accession: S47382
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35687; NID:G527463; PIDN:CAA84756.1; PID:G527464; EMBL:Z35695;
C;Keywords: T-cell receptor

Query Match 35.4%; Score 25.5; DB 2; Length 13;
Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
|||: |||:
Db 1 CASSM-RSTD 10

RESULT 15
S23371
T-cell receptor alpha chain J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S23371
R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman
Eur. J. Immunol. 21, 2749-2754, 1991
A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu
A;Reference number: S23364; MUID:92037820; PMID:1657615
A;Accession: S23371
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-10 <PLU>
A;Cross-references: EMBL:X58166
C;Keywords: T-cell receptor

Query Match 34.7%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGKST 9
: |||||
Db 2 SGEAGKST 9

Search completed: September 5, 2004, 10:32:20
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:20:35 ; Search time 15 Seconds
(without alignments)
45.127 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 597

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	23	31.9	12	1	PSP3 PHYPA
2	20	27.8	12	1	V23K WSSV
3	20	27.8	13	1	LIGA TRAVE
4	20	27.8	13	1	PSPB PINPS
5	19	26.4	10	1	COXM RAT
6	18	25.0	12	1	UR2B CATCO
7	18	25.0	13	1	FARB ASCSU
8	17	23.6	12	1	UR2B CYPCA
9	16	22.2	9	1	XYLA STRSQ
10	16	22.2	11	1	TKC2 CALVO
11	16	22.2	12	1	CLX3 CONMR
12	16	22.2	12	1	TA10 TREME
13	16	22.2	13	1	CXAA CONST
14	16	22.2	13	1	HPB9 RANES
15	15	20.8	9	1	CCAP CARMA
16	15	20.8	9	1	FAR5 ASCSU
17	15	20.8	9	1	SAMP MUSCA
18	15	20.8	9	1	SAP STOVA
19	15	20.8	10	1	COXQ RABIT
20	15	20.8	10	1	ODP2 BOVIN
21	15	20.8	11	1	CX5A CONAL
22	15	20.8	11	1	CX5B CONAL
23	15	20.8	11	1	FAR9 CALVO
24	15	20.8	11	1	TIN1 HOPTI
25	15	20.8	12	1	CXAI CONIM
26	15	20.8	12	1	NO40 LOTJA
27	15	20.8	12	1	SO15 BACSU
28	15	20.8	13	1	CRBL VESTR
29	15	20.8	13	1	CXAI CONGE
30	15	20.8	13	1	GER1 HORVU
31	15	20.8	13	1	GER2 HORVU
32	14	19.4	7	1	IGAO DACDE
33	14	19.4	7	1	UC24 MAIZE

34 14 19.4 9 1 FARB MACRS
35 14 19.4 10 1 LPK2 LOEMI
36 13 18.1 10 1 SYK CAMDP
37 13 18.1 10 1 TKL4 LOEMI
38 13 18.1 10 1 TKNB CHICK
39 13 18.1 10 1 TKNB ONCMY
40 13 18.1 10 1 TKNB RANCA
41 13 18.1 10 1 URA6 HUMAN
42 13 18.1 10 1 VEGE BACSU
43 13 18.1 12 1 UR2 POLSP
44 13 18.1 13 1 CRBL VESMA
45 13 18.1 13 1 ITB5 BOVIN

ALIGNMENTS

RESULT 1
PSP3 PHYPA STANDARD; PRT; 12 AA.
AC P80662;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEE2) (24 kDa subunit of oxygen evolving system of photosystem II) (Fragment).
DE Physcomitrella patens (Moss).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]_SEQUENCE.
RP TISSUE=Protonema;
RC MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting plastid enzymes";
RL Planta 201:261-272(1997).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex.
CC -!- INDUCTION: By light.
CC -!- SIMILARITY: Belongs to the psbp family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane; Multigene family.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C44DC5 CRC64;
Query Match 31.9%; Score 23; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 6 GKSTNTFF 12
|:|:
Db 3 GESANVF 9

RESULT 2
V23K WSSV STANDARD; PRT; 12 AA.
ID V23K WSSV
AC P82005;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 23 kDa structural polypeptide (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=92652;
RN [1]_SEQUENCE.
RP STRAIN=South Carolina;
RC MEDLINE=20214217; PubMed=10752552;
RX Wang Q., Poulos B.T., Lightner D.V.;

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RT "Protein analysis of geographic isolates of shrimp white spot syndrome
virus.";
RL Arch. Virol. 145:263-274 (2000).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON TER 12
SQ SEQUENCE 12 AA; 1323 MW; 0C0F41E91D51A724 CRC64;

Query Match 27.8%; Score 20; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ELGKSTN 10
| | |
DB 2 EFGNLTN 8

RESULT 3
LIGA TRAVE STANDARD; PRT; 13 AA.
AC P20011, 1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ligninase A (EC 1.11.1.14) (Diarylpropane peroxidase) (Lignin
peroxidase) (Fragment).
OS Trametes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=5325;
RN [1]
RP SEQUENCE.
RX MEDLINE=89211432; PubMed=2707445;
RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;
RT "Trametes versicolor ligninase: isozyme sequence homology and
substrate specificity.";
RL FEBS Lett. 247:143-146 (1989).
CC -!- FUNCTION: Depolymerization of lignin. Catalyzes the C(alpha)-
C(beta) cleavage of the propyl side chains of lignin.
CC C(beta) cleavage of the propyl side chains of lignin.
CC -!- CATALYTIC ACTIVITY: 1,2-bis(3,4-dimethoxyphenyl)propane-1,3-diol +
H2O(O2) = veratraldehyde + 1-(3,4-dimethoxyphenyl)ethane-1,2-diol
+ 4 H(2)O.
CC + 4 H(2)O.
CC -!- PATHWAY: Lignin degradation; first step.
CC -!- SIMILARITY: Belongs to the peroxidase family. Ligninase subfamily.
DR PIR; S04013; S04013.
DR InterPro; IPR002016; Peroxidase.
DR PROSITE; PS00435; PEROXIDASE_1; PARTIAL.
DR PROSITE; PS00436; PEROXIDASE_2; PARTIAL.
KW Oxidoreductase; Peroxidase; Iron; Heme; Glycoprotein;
KW Multigene family; Lignin degradation.
FT NON TER 13
SQ SEQUENCE 13 AA; 1298 MW; 22C50ED5872A4338 CRC64;

Query Match 27.8%; Score 20; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 GKSTNT 11
| | |
DB 6 GKNTAT 11

RESULT 4
PSBP_PINPS STANDARD; PRT; 13 AA.
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 43, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEE2) (23 kDa subunit of oxygen
evolving system of photosystem II) (Fragment).
DE evolving system of photosystem II) (Fragment).
GN PSBP.
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RX TISSUE=Needle;
RX MEDLINE=9274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins.";
RL Electrophoresis 20:1098-1108 (1999).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex (By similarity).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N179) is: 5.9, its MW is: 22 kDa.
CC -!- SIMILARITY: Belongs to the psbp family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
FT NON TER 13
SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;

Query Match 27.8%; Score 20; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTF 12
| | |
DB 3 GERANVF 9

RESULT 5
COXM RAT STANDARD; PRT; 10 AA.
ID _COXM_RAT
AC P80431;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide Viib, mitochondrial (EC 1.9.3.1)
DE (Fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
amino-terminal sequences suggest identity of the fetal heart and the
adult liver isoform.";
RL Eur. J. Biochem. 230:235-241 (1995).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
chains of cytochrome c oxidase, the terminal oxidase in
mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferrocycytochrome
c + 2 H(2)O.
CC PIR; S65387; S65387.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 26.4%; Score 19; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 KSTNTF 12
| | |
DB 4 KKTPTF 9

RESULT 6

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UR2B_CATCO
ID UR2B_CATCO STANDARD; PRT; 12 AA.
AC P04559;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Urotensin IIB (U-IIB) (UIIB).
OS Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Catostomidae; Catostomus.
OX NCBI_TaxID=7971;
RN [1]
RP SEQUENCE.
RX MEDLINE=84041959; PubMed=6138759;
RA McMaster D., Lederis K.;
RT "Isolation and amino acid sequence of two urotensin II peptides from
RT Catostomus commersoni urophyses.";
RL Peptides 4:367-373(1983).
CC -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC PIR; JS0424; JS0424.
DR InterPro; IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1437 MW; 73961BDB879CEBB CRC64;

Query Match 25.0%; Score 18; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 TMTFC 13
Db :|||
2 SNTFC 6

RESULT 7
FARB_ASCSU
ID FARB_ASCSU STANDARD; PRT; 13 AA.
AC P43173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF11.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D6886B05 CRC64;

Query Match 25.0%; Score 18; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 SELGKSTWTF 12
Db :|||
1 SDIGISEPNF 10

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RESULT 8
UR2B_CYPCA
ID UR2B_CYPCA STANDARD; PRT; 12 AA.
AC P04561;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Urotensin II-beta (UII-beta) (U-II-beta).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RX MuneKata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
RL (In) Rich D.H., Gross E. (eds.);
RL Proceedings of the 7th American peptide symposium, pp.69-72,
RL Pierce Chemical Co., Rockford IL. (1981).
CC -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the urotensin 2 family.
DR InterPro; IPR001483; Urotensin_II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
FT VARIANT 2 2 G -> S.
SQ SEQUENCE 12 AA; 1407 MW; 73960A9FB879CEBB CRC64;

Query Match 23.6%; Score 17; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 NTFC 13
Db :|||
3 NTEC 6

RESULT 9
XYLA_STRSQ
ID XYLA_STRSQ STANDARD; PRT; 9 AA.
AC P19149;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Xylose isomerase (EC 5.3.1.5) (Fragment).
GN XYLA.
OS Streptomyces sp. (strain NCL 82-5-1).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE.
RX MEDLINE=88326335; PubMed=3415697;
RA Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
RT "Purification and characterisation of glucose (xylose) isomerase from
RT Chainia sp. (NCL 82-5-1).";
RL Biochem. Biophys. Res. Commun. 155:411-417(1988).
CC -!- FUNCTION: Involved in D-xylose catabolism.
CC -!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
CC -!- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the xylose isomerase family.
DR PIR; A31576; A31576.
DR HAMAP; MF_00455; -; 1.
DR InterPro; IPR001998; Xylose_isom.
DR PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.

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DR PROSITE: PS00173; XYLOSE ISOMERASE 2; PARTIAL.
 KW Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 983 MW; F64BA1EDC5B87DD1 CRC64;

Query Match 22.2%; Score 16; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 8 STNTF 12
 Db 5 SAHTF 9

RESULT 10
 TKC2_CALVO STANDARD; PRT; 11 AA.
 AC P415T8;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin II.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 [1]
 RN SEQUENCE, AND SYNTHESIS.
 RP MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
 RA Naessel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 RT the blowfly, Calliphora vomitoria, that have resemblances to
 RT tachykinins."
 RL Peptides 15:761-768(1994).
 CC -|- FUNCTION: Myoactive peptide.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11
 SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDB444 CRC64;

Query Match 22.2%; Score 16; DB 1; Length 11;
 Best Local Similarity 42.9%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 6 GKSTNTF 12
 Db 1 GLGNNAF 7

RESULT 11
 CXL3_CONMR STANDARD; PRT; 12 AA.
 AC P58809;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda-conotoxin CmrX.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 [1]
 RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RP TISSUE=Venom.
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji R.A., Ohake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the

RT venom of Conus marmoreus.";
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -|- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -|- MASS SPECTROMETRY: MW=1262.77; MW ERR=0.07; METHOD=Electrospray.
 CC -|- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 3 12
 FT DISULFID 4 9
 FT MOD_RES 11 11 HYDROXYLATION.
 SQ SEQUENCE 12 AA; 1251 MW; 277AAAE2422DSA2C8 CRC64;

Query Match 22.2%; Score 16; DB 1; Length 12;
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TFC 13
 Db 7 SFC 9

RESULT 12
 TAL0_TREME STANDARD; PRT; 12 AA.
 AC P01371;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tremorgen A-10.
 OS Tremella mesenterica (Jelly fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Tremella.
 OX NCBI_TaxID=5217;
 [1]
 RN SEQUENCE.
 RA Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
 RT "Peptide sex hormones inducing conjugation tube formation in
 RT compatible mating-type cells of Tremella mesenterica."
 RL Science 212:1525-1527(1981).
 CC -|- FUNCTION: Tremorgen A-10 is produced by the a mating-type cells
 CC and induces formation of conjugation tubes in a mating-type cells.
 DR PIR; A01642; JTJGO.
 KW Lipoprotein; Prenylation; Methylation; Pheromone.
 FT LIPID 12 12 S-12-hydroxyfarnesyl cysteine.
 FT MOD_RES 12 12 METHYLATION.
 SQ SEQUENCE 12 AA; 1246 MW; 84EF574959676DC5 CRC64;

Query Match 22.2%; Score 16; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 6.2e+03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 NTFC 13
 Db 9 NGYC 12

RESULT 13
 CXAA_CONST STANDARD; PRT; 13 AA.
 AC P28878;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin SIA (SIA).
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6493;
 [1]
 RN SEQUENCE.
 RP TISSUE=Venom;

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RX MEDLINE=91369955; PubMed=1892838;
RA Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
RA Oliveira B.M.;
RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
RT receptors.";
RL Biochemistry 30:9370-9377(1991).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR: A40312; NTKNAS.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 7
FT MOD RES 3 13
FT NON RES 13 13
SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

Query Match 22.2%; Score 16; DB 1; Length 13;
Best Local Similarity 37.5%; Pred. No. 6.7e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELCKS 8
Db | | |
3 CHPACGKN 10

RESULT 14
HPB9 RANES STANDARD; PRT; 13 AA.
AC P32416;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein B9 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90198965; PubMed=2317508;
RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: Shows hemolytic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR: S09019; S09019.
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD RES 13 13
FT NON RES 13 13
SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 22.2%; Score 16; DB 1; Length 13;
Best Local Similarity 56.7%; Pred. No. 6.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELCK 7
Db | | |
6 AGLCK 11

RESULT 15
CCAP CARMA STANDARD; PRT; 9 AA.
ID CCAP CARMA
AC P38556;

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DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexta; PubMed=1426284;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.-C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: The effect of CCAP is both ino- and chronotropic.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Stored in pericardial organs and released
CC into the hemolymph.
DR PIR: A26363; A26363.
DR PIR: S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 20.8%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FC 13
Db | |
2 FC 3

Search completed: September 5, 2004, 10:30:49
Job time : 16 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:22:06 ; Search time 57 Seconds
(without alignments)
71.960 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3001

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertibrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	37.5	13	13 Q8QZ5	Q8QZ5 fugu rubrip
2	26	36.1	13	12 Q9184	Q9184 human papil
3	26	36.1	13	12 Q9186	Q9186 human papil
4	23	31.9	12	13 Q9PS67	Q9PS67 gallus gall
5	21	29.2	12	12 Q85666	Q85666 reovirus (t
6	21	29.2	13	6 Q8GJU2	Q8GJU2 ovis aries
7	21	29.2	13	13 P82821	P82821 rana catesb
8	21	29.2	13	13 P82822	P82822 rana catesb
9	20	27.8	11	10 Q9T0L9	Q9T0L9 brassica ol
10	20	27.8	12	3 Q9UR22	Q9UR22 cryptococu
11	20	27.8	12	13 P82820	P82820 rana catesb
12	20	27.8	13	11 Q80W20	Q80W20 rattus sp.
13	20	27.8	13	13 P82823	P82823 rana catesb
14	19	26.4	12	11 Q61331	Q61331 mus musculu
15	19	26.4	13	11 Q54809	Q54809 mus musculu
16	18	25.0	8	7 Q95213	Q95213 oryctolagus

17	18	25.0	11	9	Q37925	Q37925 bacterioph
18	18	25.0	11	13	Q9PS71	Q9PS71 agkistrodon
19	18	25.0	12	6	Q7YS46	Q7YS46 ovis aries
20	18	25.0	12	8	Q7YKE9	Q7YKE9 ribes divar
21	18	25.0	13	4	Q9UDC6	Q9UDC6 homo sapien
22	18	25.0	13	13	P82881	P82881 rana clamit
23	17	23.6	11	2	Q9EUZ3	Q9EUZ3 escherichia
24	17	23.6	11	4	Q9HCN5	Q9HCN5 homo sapien
25	17	23.6	12	5	Q8T0Y6	Q8T0Y6 apis mellif
26	17	23.6	12	6	Q9BFV4	Q9BFV4 myrmecophag
27	17	23.6	12	8	Q7YKC9	Q7YKC9 ribes speci
28	17	23.6	13	4	Q13377	Q13377 homo sapien
29	17	23.6	13	11	Q35758	Q35758 rattus norv
30	16	22.2	8	2	Q7X139	Q7X139 staphylococ
31	16	22.2	9	2	Q30790	Q30790 erwinia amy
32	16	22.2	9	4	Q15999	Q15999 homo sapien
33	16	22.2	9	12	Q88612	Q88612 middelburg
34	16	22.2	10	4	Q8NEY9	Q8NEY9 homo sapien
35	16	22.2	10	6	Q9TRU6	Q9TRU6 bos taurus
36	16	22.2	11	11	P97330	P97330 mus musculu
37	16	22.2	11	11	Q9RLN6	Q9RLN6 mus musculu
38	16	22.2	12	2	Q9S550	Q9S550 streptococ
39	16	22.2	12	5	Q17140	Q17140 crassostrea
40	16	22.2	12	5	Q26429	Q26429 drosophila
41	16	22.2	12	11	Q64242	Q64242 rattus sp.
42	16	22.2	13	4	Q9UME9	Q9UME9 homo sapien
43	16	22.2	13	4	Q9GQ66	Q9GQ66 homo sapien
44	16	22.2	13	5	Q818F2	Q818F2 drosophila
45	16	22.2	13	5	Q818F1	Q818F1 drosophila

ALIGNMENTS

RESULT 1

Q8QZ5	PRELIMINARY;	PRT;	13 AA.
ID	Q8QZ5		
AC	Q8QZ5;		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Guanine nucleotide binding protein (Fragment).		
GN	GNAO.		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
OC	Tetraodontidae; Tetraodontidae; Takifugu.		
OX	NCBI_TaxID=31033;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97129408; PubMed=8973916;		
RA	Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;		
RT	"G protein alpha subunit multigene family in the Japanese puffer fish		
RT	Fugu rubripes; PCR from a compact vertebrate genome.";		
RL	Genome Res. 6:1207-1215(1996).		
DR	EMBL; L79891; AAL77640.1;		
DR	GO; GO:0004871; F:signal transducer activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.		
DR	InterPro; IPR001019; Gprotein_alpha.		
DR	Pfam; PF00503; G-alpha; 1.		
FT	NON_TER 1		
FT	NON_TER 13		
SQ	SEQUENCE 13 AA; 1336 MW; 465B59640B44B5B3 CRC64;		

Query Match 37.5%; Score 27; DB 13; Length 13;

Best Local Similarity 75.0%; Pred. No. 3.6e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASELGSKT 9

Db 1 AGESGSKT 8

```

RESULT 2
Q918T4 PRELIMINARY; PRT; 13 AA.
AC Q918T4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC7;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407220; AAL01406.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 36.1%; Score 26; DB 12; Length 13;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
DB 4 CVS--GQNTNT 12

RESULT 3
Q918T6 PRELIMINARY; PRT; 13 AA.
AC Q918T6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC6;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407219; AAL01403.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 36.1%; Score 26; DB 12; Length 13;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
DB 4 CVS--GQNTNT 12

RESULT 4
Q9P867 PRELIMINARY; PRT; 12 AA.
ID Q9P867
AC Q9P867;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

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DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Myosin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92031443; PubMed=1931944;
RA Garabedian T.B., Yount R.G.;
RT "Direct photoaffinity labeling of gizzard myosin with vanadate-trapped
RT adenosine diphosphate.";
RL Biochemistry 30:10126-10132(1991).
DR PIR; A23695; A23695.
FT NON TER 1
SQ SEQUENCE 12 AA; 1178 MW; C1FC2E0D9AA3387D CRC64;

Query Match 31.9%; Score 23; DB 13; Length 12;
Best Local Similarity 55.6%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SELGKSTNT 11
DB 3 SGAGKTENT 11

RESULT 5
Q85666 PRELIMINARY; PRT; 12 AA.
ID Q85666
AC Q85666;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Reovirus serotype 3 M3 (Fragment).
OS Reovirus (type 3 / strain Dearing).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10886;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017876; PubMed=6927854;
RA Antczak J.B., Chmelo R., Pickup D.J., Joklik W.K.;
RT "Sequences at both termini of the 10 genes of reovirus serotype 3
RT (strain Dearing).";
RL Virology 121:307-319(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017877; PubMed=7123853;
RA Gaillard R.K., Li J.K., Keene J.D., Joklik W.K.;
RT "The sequences at the termini of four genes of the three reovirus
RT serotypes.";
RL Virology 121:320-326(1982).
DR EMBL; J02323; AAA47259.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1275 MW; 4B292B17FCB9C873 CRC64;

Query Match 29.2%; Score 21; DB 12; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.6e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ASELGKSTNT 11
DB 2 ASFKGFSANT 11

RESULT 6
Q9GJU2 PRELIMINARY; PRT; 13 AA.
ID Q9GJU2
AC Q9GJU2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

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DE Calpastatin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Nonneman D., Geesink G.H., Koohmaraie M.;
RT "Differential splicing and protein isoforms of ovine calpastatin.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF192536; AAG31688.1; -.
DR EMBL; AF192535; AAG31687.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1335 MW; 47E9542C696BADD3 CRC64;

Query Match 29.2%; Score 21; DB 6; Length 13;
Best Local Similarity 80.0%; Pred. No. 5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GKSTN 10
DB 9 GKSTS 13

RESULT 7
P82821 ID P82821 PRELIMINARY; PRT; 13 AA.
AC P82821;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RANATUERIN 6.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranaturins; antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592 (1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
DR GO; GO:0006805; P: xenobiotic metabolism; IEA.
KW Antibiotic.
SQ SEQUENCE 13 AA; 1398 MW; C85480BD0CF885BD CRC64;

Query Match 29.2%; Score 21; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGK 7
DB 6 ASMLGK 11

RESULT 8
P82822 ID P82822 PRELIMINARY; PRT; 13 AA.
AC P82822;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RANATUERIN 7.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;

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RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranaturins; antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592 (1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
DR GO; GO:0006805; P: xenobiotic metabolism; IEA.
KW Antibiotic.
SQ SEQUENCE 13 AA; 1398 MW; C85480BD0CF885BD CRC64;

Query Match 29.2%; Score 21; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGK 7
DB 6 ASMLGK 11

RESULT 9
Q9T0L9 ID Q9T0L9 PRELIMINARY; PRT; 11 AA.
AC Q9T0L9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SLG5 protein (Fragment).
GN SLG5.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99264316; PubMed=10330480;
RA Caballiac D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
RA Dumas C., Gaude T., Cock J.M.;
RT "The SL5 self-incompatibility haplotype in Brassica includes three S
RT gene family members which are expressed in stigmas.";
RL Plant Cell 11:971-986 (1999).
DR EMBL; Y18256; CAB41875.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1035 MW; CD3806DDA8772AAD CRC64;

Query Match 27.8%; Score 20; DB 10; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGKST 9
DB 3 AADLGTCT 10

RESULT 10
Q9UR22 ID Q9UR22 PRELIMINARY; PRT; 12 AA.
AC Q9UR22;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE STL2 alpha (Fragment).
GN STL2ALPHA.
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CBS884, BAL 3, and CBS6989;
RX MEDLINE=99380307; PubMed=1049476;
RA Halliday C.L., Bui T., Krockenberger M., Malik R., Ellis D.H.,
Carter D.A.;
RT "Presence of alpha and a mating types in environmental and clinical
collections of *Cryptococcus neoformans* var. *gattii* strains from
Australia";
RL J. Clin. Microbiol. 37:2920-2926(1999).
DR EMBL; AF155349; AAF20374.1; -;
DR EMBL; AF155347; AAF20372.1; -;
DR EMBL; AF155348; AAF20373.1; -;
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1307 MW; 5AF9B485D5A735B7 CRC64;
Query Match 27.8%; Score 20; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TFC 13
Db 8 TFC 10
RESULT 11
P82820 PRELIMINARY; PRT; 12 AA.
AC P82820;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE RANATUERIN 5.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Gorava J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
American bullfrog, *Rana catesbeiana*";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -!- SUBCELLULAR LOCATION: SECRETED.
SQ SEQUENCE 12 AA; 1335 MW; C8531D12A92735BD CRC64;
Query Match 27.8%; Score 20; DB 13; Length 12;
Best Local Similarity 83.3%; Pred. No. 7.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ASELGK 7
Db 5 ASLLGK 10
RESULT 12
Q80WZ0 PRELIMINARY; PRT; 13 AA.
AC Q80WZ0;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE GTP-binding protein Golf alpha subunit (Fragment).
GN G-ALPHA-OLF.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96115117; PubMed=7494450;

RA Herve D., Rogard M., Levi-Strauss M.;
RT "Molecular analysis of the multiple Golf alpha subunit mRNAs in the
rat brain";
RL Brain Res. Mol. Brain Res. 32:125-134(1995).
DR EMBL; S80330; AAB32222.1; -;
FT NON_TER 13 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1312 MW; 0B6E3319671CA5B4 CRC64;
Query Match 27.8%; Score 20; DB 11; Length 13;
Best Local Similarity 57.1%; Pred. No. 7.7e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 LGKSTNT 11
Db 4 LGSSKT 10
RESULT 13
P82823 PRELIMINARY; PRT; 13 AA.
AC P82823;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE RANATUERIN 8.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Gorava J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
American bullfrog, *Rana catesbeiana*";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
DR GO: GO:0006805; P: xenobiotic metabolism; IEA.
KW Antibiotic.
SQ SEQUENCE 13 AA; 1414 MW; C85480BD0CF7D5BD CRC64;
Query Match 27.8%; Score 20; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ASELGK 7
Db 6 ASFLGK 11
RESULT 14
Q61331 PRELIMINARY; PRT; 12 AA.
AC Q61331;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE N-acetylglucosamine (Beta1-4) galactosyl transferase (EC 2.4.1.90)
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89033997; PubMed=3141392;
RA Nakazawa K., Ando T., Kimura T., Narimatsu H.;
RT "Cloning and sequencing of a full-length cDNA of mouse N-
acetylglucosamine (beta1-4)galactosyltransferase";
RL J. Biochem. 104:165-168(1988).

Search completed: September 5, 2004, 10:31:54
Job time : 59 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:01:30 ; Search time 65 Seconds
(without alignments)
56.510 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 383904

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	13	4 AAU04524	AAU04524 VEGF base
2	69	95.8	13	4 AAU04534	AAU04534 VEGF base
3	65	90.3	13	4 AAU04535	AAU04535 VEGF base
4	65	90.3	13	4 AAU04537	AAU04537 VEGF base
5	61	84.7	13	4 AAU04536	AAU04536 VEGF base
6	32	44.4	12	3 AAY57039	AAY57039 Feline im
7	32	44.4	13	5 ABJ04094	ABJ04094 Immunoglo
8	30	41.7	13	3 AAY66781	AAY66781 T cell an
9	29	40.3	10	4 AAB75626	AAB75626 HLA class
10	29	40.3	13	3 AAY66787	AAY66787 T cell an
11	29	40.3	13	5 ABJ04095	ABJ04095 Immunoglo
12	28	38.9	9	2 AAY48678	AAY48678 Membrane
13	28	38.9	9	3 AAB10896	AAB10896 Human 9p7
14	28	38.9	9	5 AAE26783	AAE26783 Fibrin bi
15	28	38.9	10	3 AAB10895	AAB10895 Human 9p7
16	28	38.9	13	5 ABJ04091	ABJ04091 Immunoglo
17	28	38.9	13	5 ABJ04088	ABJ04088 Immunoglo
18	27	37.5	9	5 ABJ04570	ABJ04570 Bone marr
19	27	37.5	10	2 AAW42705	AAW42705 Antigenic
20	27	37.5	10	4 AAM43317	AAM43317 Mycoplasma
21	27	37.5	12	2 AAW34877	AAW34877 Human tau
22	27	37.5	12	2 AAW34865	AAW34865 Human tau
23	27	37.5	12	4 AAU28829	AAU28829 DPI trypt
24	27	37.5	12	4 AAU26477	AAU26477 Depressio
25	27	37.5	12	5 ABG67372	ABG67372 Human ADP

ALIGNMENTS

RESULT 1
ID AAU04524 standard; peptide; 13 AA.
XX
AC AAU04524;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 1.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..13
FT /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

26 27 37.5 12 6 ADA23476
27 27 37.5 13 3 AAB26567
28 27 37.5 13 4 AAU16900
29 27 37.5 13 5 ABJ00485
30 27 37.5 13 5 ABJ04090
31 27 37.5 13 5 ABJ04092
32 27 37.5 13 5 ABJ04093
33 26 36.1 8 4 AAU08458
34 26 36.1 9 2 AAW83264
35 26 36.1 9 2 AAW67159
36 26 36.1 9 2 AAW97980
37 26 36.1 9 3 AAY76718
38 26 36.1 9 6 ABP74688
39 26 36.1 9 7 ADC09547
40 26 36.1 10 4 AAG84316
41 26 36.1 10 4 AAG96997
42 26 36.1 10 4 AAG96549
43 26 36.1 10 5 ABP47552
44 26 36.1 10 6 ABP74689
45 26 36.1 10 7 ADC09548

Ada23476 Alzheimer
Aab26567 Human Ige
Aau16900 Peptide #
Abj00485 Human Ige
Abj04090 Immunoglo
Abj04092 Immunoglo
Abj04093 Immunoglo
Aau08458 Peptide C
Aaw83264 NPF motif
Aaw67159 aPL immu
Aaw97980 Human syn
Aay76718 SCP-1 HLA
Abp74688 Human SCP
Adc09547 Epitope w
Aag84316 Arabidops
Aag96997 Human com
Aag96549 Human com
Abp47552 N. mening
Abp74689 Human SCP
Adc09548 Epitope w

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 72; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
 |||||
 Db 1 CASELGKSTNTFC 13

RESULT 2
 AAU04534
 ID AAU04534 standard; peptide; 13 AA.
 XX
 AC AAU04534;
 XX
 XX 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 12.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 XX Disulfide-bond 1. .13
 FT /note= "This bond cyclises the peptide"
 XX
 XX WO200152875-A1.

XX 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 XX WPI; 2001-442248/47.
 DR

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT

PT residues.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;

Query Match 95.8%; Score 69; DB 4; Length 13;
 Best Local Similarity 92.3%; Pred. No. 6.8e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
 |||||
 Db 1 CASELGKSTNTFC 13

RESULT 3
 AAU04535
 ID AAU04535 standard; peptide; 13 AA.
 XX
 AC AAU04535;
 XX
 XX 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 13.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 XX Disulfide-bond 1. .13
 FT /note= "This bond cyclises the peptide"
 XX
 XX WO200152875-A1.

XX 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX

PA (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 25; Page 47; 102pp; English.
 PS
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 XX Sequence 13 AA;
 XX
 XX Query Match 90.3%; Score 65; DB 4; Length 13;
 XX Best Local Similarity 84.6%; Pred. No. 0.00033;
 XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGGKSTNTFC 13
 DB |||||:|||||
 1 CASELGGKSTNTFC 13
 RESULT 4
 ID AAU04537 standard; peptide; 13 AA.
 XX AAU04537;
 XX 26-SEP-2001 (first entry)
 XX VEGF based monocyclic peptide 15.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
 XX diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..13
 FT /note= "This bond cyclises the peptide"
 XX

PN WO200152875-A1.
 XX 26-JUL-2001.
 XX 18-JAN-2001; 2001WO-US001533.
 XX 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Achen MG, Hughes RA, Stacker S, Cendron A;
 PI WPI; 2001-442248/47.
 DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 25; Page 47; 102pp; English.
 PS
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 XX Sequence 13 AA;
 XX
 XX Query Match 90.3%; Score 65; DB 4; Length 13;
 XX Best Local Similarity 84.6%; Pred. No. 0.00033;
 XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGGKSTNTFC 13
 DB |||||:|||||
 1 CASELGGKSTNTFC 13
 RESULT 5
 ID AAU04536 standard; peptide; 13 AA.
 XX AAU04536;
 XX 26-SEP-2001 (first entry)
 XX VEGF based monocyclic peptide 14.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 XX neovascularisation; lymphangiogenesis; psoriasis; tumour;

AAV57039
ID AAV57039 standard; peptide; 12 AA.

XX 08-NOV-2001; 2001WO-EP012933.
 XX
 PR 08-NOV-2000; 2000EP-00124418.
 XX
 XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX
 PI Egner R, Winkler D, Roenspeck W, Kunze R;
 XX
 XX WPI; 2002-557447/59.
 XX
 XX New immunoglobulin-binding peptides, useful for removing autoantibodies
 PT from serum, e.g. for treating rheumatism, also related solid phases.
 PT
 XX Claim 3; Page 40; 54pp; German.
 PS
 XX The present invention relates to immunoglobulin binding peptides. These
 CC can be used to remove autoantibodies from solutions, particularly
 CC autoantibodies associated with autoimmune diseases such as rheumatism,
 CC multiple sclerosis and myasthenia gravis, from body fluids. The present
 CC sequence is a peptide of the invention
 XX
 XX Sequence 13 AA;
 SQ

Query Match 44.4%; Score 32; DB 5; Length 13;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CASELGK 7
 DB |||||
 2 CASHLGK 8

RESULT 8
 AAY66781
 ID AAY66781 standard; peptide; 13 AA.
 XX
 AC AAY66781;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE T cell antigen receptor Vbeta 5 chain peptide.
 XX
 DE Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
 KW Vbeta chain; autoantigen; immunological tolerance.
 KW
 XX Homo sapiens.
 OS
 XX WO9963084-A1.
 PN
 XX 09-DEC-1999.
 PD
 XX 28-MAY-1999; 99WO-JP002814.
 PF
 XX 29-MAY-1998; 98JP-00149855.
 PR
 XX 14-OCT-1998; 98JP-00328761.
 FR
 XX (TORI) TORII PHARM CO LTD.
 PA
 XX Nishioka K, Yoshino S;
 PI
 XX WPI; 2000-086978/07.
 DR
 XX N-PSDB; AA296511.
 DR

T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in
 PT synovial membranes of rheumatoid arthritis patients.
 PT
 XX Example 3; Page 25; 136pp; Japanese.
 PS
 XX The invention relates to peptide sequences present in the synovial fluid
 CC and membranes of rheumatoid arthritis patients, arising from the CDR
 CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
 CC Compositions which contain autoantigenic peptides binding specifically to

CC T-cells expressing receptors containing the peptide sequences, which
 CC include antigen-specific immunological tolerance to rheumatoid arthritis
 CC can be used for the treatment and prevention of rheumatoid arthritis. The
 CC invention can be used for the diagnosis, treatment and prevention of
 CC rheumatoid arthritis. Sequences AAY66771-958 represent peptides from the
 CC various Vbeta chains of T cell antigen receptor
 XX
 XX Sequence 13 AA;
 SQ

Query Match 41.7%; Score 30; DB 3; Length 13;
 Best Local Similarity 41.7%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 1 CASELGKSTNTP 12
 DB |||||:
 2 CASSIGTNEQF 13

RESULT 9
 AAB75626
 ID AAB75626 standard; peptide; 10 AA.
 XX
 AC AAB75626;
 XX
 DT 10-APR-2001 (first entry)
 XX
 DE HLA class I binding motif in HOM-TES-84 SEQ ID NO:29.
 XX
 KW Human; cancer associated antigen precursor; cancer associated antigen;
 KW seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
 KW vaccine; cancer.
 KW
 XX Homo sapiens.
 OS
 XX WO200100874-A2.
 PN
 XX 04-JAN-2001.
 PD
 XX 23-JUN-2000; 2000WO-US017207.
 PF
 XX 30-JUN-1999; 99US-00346498.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Sahin U, Tureci O, Pfreundschuh M;
 PI
 XX WPI; 2001-112465/12.
 DR

Diagnosing a disorder characterized by expression of a human cancer
 PT associated antigen precursor, comprises detecting interaction of an agent
 PT with a nucleic acid molecule encoding the antigen precursor.
 XX
 XX Example 10; Page 62; 136pp; English.
 PS
 XX The present invention describes a method for diagnosing a disorder
 CC characterised by expression of a human cancer associated antigen (CAA)
 CC precursor (I) coded by a NA Group 1 nucleic acid molecule (N1) comprising
 CC contacting the biological sample with an agent (A) that specifically
 CC binds to N1, (I) or its fragment, complexed with an human leukocyte
 CC antigen (HLA) molecule and determining the interaction between the agent
 CC and N1 or (I). (I) has cytostatic activity and can be used in gene
 CC therapy and vaccine production. The method can be used for treating a
 CC subject with a condition characterised by expression of (I) in cells of a
 CC subject. AAB75607 and AAB75608 represent proteins from human cancer
 CC associated antigen precursors, and AAB75609 to AAB75802 represent HLA
 CC class I binding motifs in human cancer associated antigen precursors
 CC given in the exemplification of the present invention
 XX
 XX Sequence 10 AA;
 SQ

Query Match 40.3%; Score 29; DB 4; Length 10;
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 ELKSTNTFC 13
: ||| ||| |
Db 1 KLGSFNTNC 10

RESULT 10
AAY66787
ID AAY66787 standard; peptide; 13 AA.

XX AC AAY66787;
XX DT 11-APR-2000 (first entry)
XX XX

DE T cell antigen receptor Vbeta 10 chain peptide.

XX Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
KW Vbeta chain; autoantigen; immunological tolerance.

XX Homo sapiens.

XX WO963084-A1.

XX 09-DEC-1999.

XX 28-MAY-1999; 99WO-JP002814.

XX 29-MAY-1998; 98JP-00149855.

XX 14-OCT-1998; 98JP-00328761.

XX (TORI) TORII PHARM CO LTD.

XX Nishioka K, Yoshino S;

XX WPI; 2000-086978/07.

XX N-PSDB; AA296517.

XX T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in

XX synovial membranes of rheumatoid arthritis patients.

XX Example 3; Page 29; 136pp; Japanese.

XX The invention relates to peptide sequences present in the synovial fluid
CC and membranes of rheumatoid arthritis patients, arising from the CDR
CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
CC Compositions which contain autoantigenic peptide binding specifically to
CC T-cells expressing receptors containing the peptide sequences, which
CC include antigen-specific immunological tolerance to rheumatoid arthritis
CC can be used for the treatment and prevention of rheumatoid arthritis. The
CC invention can be used for the diagnosis, treatment and prevention of
CC rheumatoid arthritis. Sequences AAY66771-958 represent peptides from the
CC various Vbeta chains of T cell antigen receptor

XX SQ Sequence 13 AA;

Query Match 40.3%; Score 29; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CASELGKST 9
||| ||| |
Db 2 CASSKGTST 10

RESULT 11
ABJ04095
ID ABJ04095 standard; peptide; 13 AA.

XX AC ABJ04095;

XX 01-OCT-2002 (first entry)

XX Immunoglobulin binding peptide #15.

XX Immunoglobulin binding peptide; autoimmune disease; rheumatoid arthritis;
KW multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic;
KW neuroprotective.

XX Synthetic.

XX WO200238592-A2.

XX 16-MAY-2002.

XX 08-NOV-2001; 2001WO-EP012933.

XX 08-NOV-2000; 2000EP-00124418.

XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.

XX Egner R, Winkler D, Roenspeck W, Kunze R;

XX WPI; 2002-557447/59.

XX New immunoglobulin-binding peptides, useful for removing autoantibodies
PT from serum, e.g. for treating rheumatism, also related solid phases.

XX Claim 3; Page 40; 54pp; German.

XX The present invention relates to immunoglobulin binding peptides. These
CC can be used to remove autoantibodies from solutions, particularly
CC autoantibodies associated with autoimmune diseases such as rheumatism,
CC multiple sclerosis and myasthenia gravis, from body fluids. The present
CC sequence is a peptide of the invention

XX SQ Sequence 13 AA;

Query Match 40.3%; Score 29; DB 5; Length 13;

Best Local Similarity 71.4%; Pred. No. 4.5e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7

Db 2 CATHLCK 8

RESULT 12

AAAY48678

ID AAY48678 standard; peptide; 9 AA.

XX AC AAY48678;

XX 20-MAR-2003 (revised)

DT 10-DEC-1999 (first entry)

XX Membrane dipeptidase-binding lung homing peptide #49.

XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;

XX prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;

XX membrane dipeptidase.

XX Synthetic.

XX Homo sapiens.

XX WO9946284-A2.

XX 16-SEP-1999.

XX 10-MAR-1999; 99WO-US005284.

XX 13-MAR-1998; 98US-00042107.

XX 26-FEB-1999; 99US-00258754.

XX (BURN-) BURNHAM INST.

XX Rajotte D, Pasqualini R, Ruoslahti EI;

XX WPI; 1999-571717/48.
 XX New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.
 XX Example 6; Page 144; 193pp; English.
 XX The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue, for identifying a target molecule expressed by an organ or tissue
 CC or for treating an organ or tissue pathology, where the organ or tissue
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
 CC used in the exemplification of the present invention. (Updated on 20-MAR-
 CC 2003 to correct PR field.)
 XX Sequence 9 AA;
 SQ Query Match 38.9%; Score 28; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KSTNTFC 13
 DB :|||||
 3 RSTNTGC 9
 RESULT 13
 AAB10896
 ID AAB10896 standard; protein; 9 AA.
 AC AAB10896;
 XX 26-JAN-2001 (first entry)
 XX Human 9D7 protein immunogenic fragment SEQ ID NO: 55.
 XX Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;
 KW immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;
 KW lung; colon; breast; carcinoma; Hodgkin's lymphoma.
 XX Homo sapiens.
 OS DE19909503-A1.
 PN 07-SEP-2000.
 PD 04-MAR-1999; 99DE-01009503.
 XX 04-MAR-1999; 99DE-01009503.
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX Klade C, Adolf G, Sommergruber W, Heider K;
 XX WPI; 2000-580357/56.
 XX New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer
 PT and for producing diagnostic or therapeutic antibodies.
 XX Claim 6; Page 45; 50pp; German.
 XX This invention describes a novel tumor-associated antigen, designated 9D7
 CC which has cytostatic activity. The invention also describes a method for
 CC isolating (a) a polypeptide (I) that includes (S1) as part of its
 CC sequence; (b) an immunogenic protein fragment or peptide (II) derived
 CC from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7,
 CC (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a
 CC protein (IV) with the immunogenic properties of 9D7 or its fragments; (e)
 CC a recombinant DNA (IIia) that includes (III); and (f) antibodies (Ab)
 CC directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

CC peptides, are used to induce a humoral and/or cellular response for use
 CC in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7
 CC can be used similarly and cells that express 9D7 are useful in cellular
 CC anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for
 CC imaging, diagnosing and monitoring cancers, also, when conjugated to
 CC cytotoxins or radionuclide, as therapeutic agents. Peptides derived from
 CC 9D7 may also be used diagnostically to test for an immune response. 9D7-
 CC associated cancers are particularly kidney, lung, colon and breast
 CC carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic
 CC fragments of the human tumor-associated antigen 9D7 which is described in
 CC the method of the invention
 XX Sequence 9 AA;
 SQ Query Match 38.9%; Score 28; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CASELCK 7
 DB :|||||
 3 CGSRLGK 9
 RESULT 14
 AAE26783
 ID AAE26783 standard; peptide; 9 AA.
 XX AAE26783;
 AC AAE26783;
 XX 13-DEC-2002 (first entry)
 XX Fibrin binding peptide #36.
 XX Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;
 KW myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic;
 KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;
 KW inflammatory disorder; angiogenesis; stroke; cerebroprotective.
 XX Unidentified.
 OS WO200255544-A2.
 PN 18-JUL-2002.
 PD 21-DEC-2001; 2001WO-US049534.
 XX 23-DEC-2000; 2000US-00747403.
 XX (DYAX-) DYAX CORP.
 PA Wescott CR, Beltzer JP, Sato AK;
 PI WPI; 2002-666875/71.
 XX Novel synthetic fibrin-binding moiety, useful for detecting, imaging or
 PT localizing fibrin-containing clots by magnetic resonance imaging,
 PT radioimaging and for treating diseases involving thrombus formation e.g.
 PT stroke.
 XX Claim 4; Page 55; 89pp; English.
 XX The invention relates to a synthetic fibrin binding group having affinity
 CC for fibrin. The invention is useful for detecting fibrin in a mammalian
 CC subject which involves (a) detectably labelling the binding group; (b)
 CC administering to the subject the labelled polypeptide, and (c) detecting
 CC the labelled polypeptide in the subject. The invention is useful for
 CC treating a disease involving thrombus formation eg. deep-vein thrombosis,
 CC pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial
 CC infarct, reperfusion ischaemia or stroke. The binding moieties are useful
 CC for detection, imaging and localisation of fibrin-containing clots by
 CC magnetic resonance imaging, radioimaging and other imaging methods and
 CC are also useful in the diagnosis and treatment of coronary conditions
 CC where fibrin plays a role. The fibrin binding moieties are useful for

CC detecting and diagnosing numerous pathophysiologies in which fibrin plays
CC a role eg. peritoneal adhesions which often occur after surgery or
CC inflammatory and neoplastic processes and are comprised of a fibrin
CC network, fibroblasts, macrophages and new blood vessels; rheumatoid
CC arthritis, lupus or septic arthritis which often have bits of fibrin
CC containing tissues called rice bodies in the synovial fluid of their
CC joints; thrombocytopenic purpura, a type of anaemia in which deposits in
CC arterioles causes turbulent blood flow resulting in stress and
CC destruction of red blood cells. The fibrin specific agents can also be
CC used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain
CC or other organs, as well as the detection of tumours, diabetic
CC retinopathy, early or high-risk atherosclerosis and other autoimmune and
CC inflammatory disorders. Fibrin specific agents also could provide both
CC direct or surrogate markers of disease models in which hypoxia and
CC angiogenesis are expected to play a role. The invention is also useful
CC for screening molecular libraries. The present sequence is a fibrin
CC binding peptide
XX
SQ Sequence 9 AA;

Query Match 38.9%; Score 28; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTFC 13
| : : : :
Db 2 GQESTTFC 9

RESULT 15
AAB10895
ID AAB10895 standard; protein; 10 AA.
XX
AC AAB10895;
XX
DT 26-JAN-2001 (first entry)
XX
DE Human 9D7 protein immunogenic fragment SEQ ID NO: 54.
XX
KW Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;
KW immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;
KW lung; colon; breast; carcinoma; Hodgkin's lymphoma.
XX
OS Homo sapiens.
XX
XX DE19909503-A1.
XX
XX 07-SEP-2000.
XX
XX 04-MAR-1999; 99DE-01009503.
XX
XX 04-MAR-1999; 99DE-01009503.
XX
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
XX Klade C, Adolf G, Sommergruber W, Heider K;
XX
XX WPI; 2000-588357/56.
XX
XX New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer
XX and for producing diagnostic or therapeutic antibodies.
XX
XX Claim 6; Page 45; 50pp; German.
XX
XX This invention describes a novel tumor-associated antigen, designated 9D7
XX which has cytostatic activity. The invention also describes a method for
XX isolating (a) a polypeptide (I) that includes (S1) as part of its
XX sequence; (b) an immunogenic protein fragment or peptide (II) derived
XX from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7,
XX (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a
XX protein (IV) with the immunogenic properties of 9D7 or its fragments; (e)
XX a recombinant DNA (IIa) that includes (III); and (f) antibodies (Ab)
XX directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

CC peptides, are used to induce a humoral and/or cellular response for use
CC in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7
CC can be used similarly and cells that express 9D7 are useful in cellular
CC anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for
CC imaging, diagnosing and monitoring cancers, also, when conjugated to
CC cytotoxins or radionuclide, as therapeutic agents. Peptides derived from
CC 9D7 may also be used diagnostically to test for an immune response. 9D7-
CC associated cancers are particularly kidney, lung, colon and breast
CC carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic
CC fragments of the human tumor-associated antigen 9D7 which is described in
CC the method of the invention
XX
SQ Sequence 10 AA;
Query Match 38.9%; Score 28; DB 3; Length 10;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELQK 7
| : : : :
Db 4 CGSRLQK 10

Search completed: September 5, 2004, 10:30:29
Job time : 67 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:32:02 ; Search time 67 Seconds
(without alignments)
61.132 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 191768

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	72	100.0	13	9 US-09-761-636A-5	Sequence 5, Appl
2	69	95.8	13	9 US-09-761-636A-15	Sequence 15, Appl
3	65	90.3	13	9 US-09-761-636A-16	Sequence 16, Appl
4	65	90.3	13	9 US-09-761-636A-18	Sequence 18, Appl
5	61	84.7	13	9 US-09-761-636A-17	Sequence 17, Appl
6	32	44.4	13	16 US-10-415-665-14	Sequence 14, Appl
7	30	41.7	10	14 US-10-208-304-14	Sequence 14, Appl
8	29	40.3	13	16 US-10-415-665-15	Sequence 15, Appl
9	28	38.9	9	14 US-10-034-974-55	Sequence 55, Appl
10	28	38.9	13	16 US-10-415-665-8	Sequence 8, Appl
11	28	38.9	13	16 US-10-415-665-11	Sequence 11, Appl
12	27	37.5	10	10 US-09-572-822C-626	Sequence 626, App
13	27	37.5	10	14 US-10-271-343-19	Sequence 19, Appl
14	27	37.5	12	10 US-09-791-393-262	Sequence 262, App
15	27	37.5	12	10 US-09-791-389-262	Sequence 262, App

16	27	37.5	12	12 US-09-142-613-22	Sequence 22, Appl
17	27	37.5	12	12 US-10-014-340-84	Sequence 84, Appl
18	27	37.5	13	12 US-10-362-527-269	Sequence 269, App
19	27	37.5	13	14 US-10-322-210-67	Sequence 67, Appl
20	27	37.5	13	14 US-10-304-443-67	Sequence 67, Appl
21	27	37.5	13	16 US-10-415-665-10	Sequence 10, Appl
22	27	37.5	13	16 US-10-415-665-12	Sequence 12, Appl
23	27	37.5	13	16 US-10-415-665-13	Sequence 13, Appl
24	26	36.1	8	9 US-09-795-006A-140	Sequence 140, App
25	26	36.1	9	15 US-10-117-937-572	Sequence 572, App
26	26	36.1	9	15 US-10-044-844-70	Sequence 70, Appl
27	26	36.1	10	10 US-09-572-404B-2743	Sequence 2743, App
28	26	36.1	10	10 US-09-572-404B-3191	Sequence 3191, App
29	26	36.1	10	10 US-09-572-270A-956	Sequence 956, App
30	26	36.1	10	12 US-10-398-104-128	Sequence 128, App
31	26	36.1	10	14 US-10-208-304-12	Sequence 12, Appl
32	26	36.1	10	14 US-10-208-304-13	Sequence 13, Appl
33	26	36.1	10	14 US-10-208-304-15	Sequence 15, Appl
34	26	36.1	10	14 US-10-208-304-16	Sequence 16, Appl
35	26	36.1	10	15 US-10-117-937-573	Sequence 573, App
36	26	36.1	11	12 US-10-398-104-153	Sequence 153, App
37	26	36.1	11	12 US-10-398-104-268	Sequence 268, App
38	26	36.1	11	16 US-10-415-665-82	Sequence 82, Appl
39	26	36.1	12	12 US-09-142-613-10	Sequence 10, Appl
40	26	36.1	12	16 US-10-415-665-66	Sequence 66, Appl
41	26	36.1	12	16 US-10-415-665-74	Sequence 74, Appl
42	26	36.1	13	10 US-09-792-686A-26	Sequence 26, Appl
43	26	36.1	13	12 US-10-609-217-170	Sequence 170, App
44	26	36.1	13	12 US-10-632-388-170	Sequence 170, App
45	26	36.1	13	12 US-10-651-723-170	Sequence 170, App

ALIGNMENTS

RESULT 1
US-09-761-636A-5
; Sequence 5, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-5

Query Match 100.0%; Score 72; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 2
US-09-761-636A-15
; Sequence 15, Application US/09761636A
; Patent No. US20020065218A1

; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-15

Query Match 95.8%; Score 69; DB 9; Length 13;
Best Local Similarity 92.3%; Pred. No. 2.2e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 3
US-09-761-636A-16
; Sequence 16, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16

Query Match 90.3%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.00011;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 4
US-09-761-636A-18
; Sequence 18, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-18

Query Match 90.3%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.00011;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 5
US-09-761-636A-17
; Sequence 17, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-17

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Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 6
US-10-415-665-14
; Sequence 14, Application US/10415665
; Publication No. US20040087765A1
; GENERAL INFORMATION:
; APPLICANT: Egner, Ralf
; APPLICANT: Kunze, Rudolf
; APPLICANT: Winkler, Dirk
; APPLICANT: Roenspeck, Wolfgang
; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for
; TITLE OF INVENTION: Binding Immunoglobulins
; FILE REFERENCE: P68842US0
; CURRENT APPLICATION NUMBER: US/10/415,665
; CURRENT FILING DATE: 2003-10-16

; PRIOR APPLICATION NUMBER: PCT/EP01/12933
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: EP00124418.5
 ; PRIOR FILING DATE: 2000-11-08
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence:
 ; OTHER INFORMATION: synthetic peptide having affinity for
 ; OTHER INFORMATION: immunoglobulins
 US-10-415-665-14

Query Match 44.4%; Score 32; DB 16; Length 13;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELKGK 7
 ||| |||
 Db 2 CASHLKGK 8

RESULT 7

US-10-208-304-14
 ; Sequence 14, Application US/10208304
 ; Publication No. US20030124571A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Larisch, Sarit
 ; APPLICANT: Kim, Seong-Jin
 ; APPLICANT: Lechleider, Robert J.
 ; APPLICANT: Roberts, Anita B.
 ; APPLICANT: Yi, Youngsuk
 ; TITLE OF INVENTION: NOVEL HUMAN SEPTIN AND USES THEREFOR
 ; FILE REFERENCE: 11613.42USW1
 ; CURRENT APPLICATION NUMBER: US/10/208,304
 ; CURRENT FILING DATE: 2002-07-29
 ; PRIOR APPLICATION NUMBER: PCT/US01/02466
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: US 60/178,866
 ; PRIOR FILING DATE: 2000-01-29
 ; PRIOR APPLICATION NUMBER: US 60/258,725
 ; PRIOR FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Drosophila
 US-10-208-304-14

Query Match 41.7%; Score 30; DB 14; Length 10;
 Best Local Similarity 87.5%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
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 Db 2 ASGLGKST 9

RESULT 8

US-10-415-665-15
 ; Sequence 15, Application US/10415665
 ; Publication No. US20040087765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Egner, Ralf
 ; APPLICANT: Kunze, Rudolf
 ; APPLICANT: Winkler, Dirk
 ; APPLICANT: Roenspeck, Wolfgang
 ; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for
 ; TITLE OF INVENTION: Binding Immunoglobulins

; FILE REFERENCE: P68842US0
 ; CURRENT APPLICATION NUMBER: US/10/415,665
 ; CURRENT FILING DATE: 2003-10-16
 ; PRIOR APPLICATION NUMBER: PCT/EP01/12933
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: EP00124418.5
 ; PRIOR FILING DATE: 2000-11-08
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence:
 ; OTHER INFORMATION: synthetic peptide having affinity for
 ; OTHER INFORMATION: immunoglobulins
 US-10-415-665-15

Query Match 40.3%; Score 29; DB 16; Length 13;
 Best Local Similarity 71.4%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELKGK 7
 ||| |||
 Db 2 CATHLKGK 8

RESULT 9

US-10-034-974-55
 ; Sequence 55, Application US/10034974
 ; Publication No. US20030143158A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DYAX CORP.
 ; APPLICANT: Beltzer, James P.
 ; APPLICANT: Wescott, Charles R.
 ; APPLICANT: Sato, Aaron K.
 ; TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS
 ; FILE REFERENCE: DYX-024.1 PCT; DYX-024.1 US
 ; CURRENT APPLICATION NUMBER: US/10/034,974
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: US 09/747,403
 ; PRIOR FILING DATE: 2000-12-23
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 55
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: fibrin binding polypeptides
 US-10-034-974-55

Query Match 38.9%; Score 28; DB 14; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.2e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTFC 13
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 Db 2 QGESRTFC 9

RESULT 10

US-10-415-665-8
 ; Sequence 8, Application US/10415665
 ; Publication No. US20040087765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Egner, Ralf
 ; APPLICANT: Kunze, Rudolf
 ; APPLICANT: Winkler, Dirk
 ; APPLICANT: Roenspeck, Wolfgang
 ; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for
 ; TITLE OF INVENTION: Binding Immunoglobulins

; FILE REFERENCE: P68842US0
; CURRENT APPLICATION NUMBER: US/10/415,665
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/EP01/12933
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: EP00124418.5
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence

; OTHER INFORMATION: Description of the artificial sequence:
; OTHER INFORMATION: synthetic peptide having affinity for
; OTHER INFORMATION: immunoglobulins
US-10-415-665-8

Query Match 38.9%; Score 28; DB 16; Length 13;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELKGK 7
|||
Db 2 CAEHLGX 8

RESULT 11

US-10-415-665-11
; Sequence 11, Application US/10415665
; Publication No. US20040087765A1

; GENERAL INFORMATION:

; APPLICANT: Egner, Ralf

; APPLICANT: Kunze, Rudolf

; APPLICANT: Winkler, Dirk

; APPLICANT: Roenspeck, Wolfgang

; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for

; TITLE OF INVENTION: Binding Immunoglobulins

; FILE REFERENCE: P68842US0

; CURRENT APPLICATION NUMBER: US/10/415,665

; CURRENT FILING DATE: 2003-10-16

; PRIOR APPLICATION NUMBER: PCT/EP01/12933

; PRIOR FILING DATE: 2001-11-08

; PRIOR APPLICATION NUMBER: EP00124418.5

; PRIOR FILING DATE: 2000-11-08

; NUMBER OF SEQ ID NOS: 88

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Description of the artificial sequence:

; OTHER INFORMATION: synthetic peptide having affinity for

; OTHER INFORMATION: immunoglobulins

US-10-415-665-11

Query Match 38.9%; Score 28; DB 16; Length 13;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELKGK 7
|||
Db 2 CAEHLGX 8

RESULT 12

US-09-573-822C-626

; Sequence 626, Application US/09573822C

; Publication No. US20030199011A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent

; CURRENT APPLICATION NUMBER: US/09/573,822C

; CURRENT FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 804

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 626

; LENGTH: 10

; TYPE: PRT

; ORGANISM: mycoplasma genitalium

; FEATURE:

; OTHER INFORMATION: Sequence located in MG309 at 847-856 and may interact with Sequen

; OTHER INFORMATION: in this patent.

US-09-573-822C-626

Query Match 37.5%; Score 27; DB 10; Length 10;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 SELGKSTNTF 12
:|:|:|:|:
Db 1 AKLSRTTNSF 10

RESULT 13

US-10-271-343-19

; Sequence 19, Application US/10271343

; Publication No. US20030166003A1

; GENERAL INFORMATION:

; APPLICANT: Cochran, Andrea G.

; APPLICANT: Skelton, Nicholas J.

; APPLICANT: Starovashnik, Melissa A.

; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES

; TITLE OF INVENTION: ON PHAGE

; FILE REFERENCE: 11669.116US11

; CURRENT APPLICATION NUMBER: US/10/271,343

; CURRENT FILING DATE: 2002-10-15

; PRIOR APPLICATION NUMBER: US 09/592,695

; PRIOR FILING DATE: 2000-06-13

; PRIOR APPLICATION NUMBER: US 60/139,017

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Turn Peptide

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (3)..(3)

; OTHER INFORMATION: Xaa is independently Trp, Tyr, Leu, Val, or Thr

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (5)..(5)

; OTHER INFORMATION: Xaa is D-pro

US-10-271-343-19

Query Match 37.5%; Score 27; DB 14; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELKGKST 9
| | | | |
Db 1 CTXEXGKLT 9

RESULT 14

US-09-791-393-262

; Sequence 262, Application US/09791393

; Publication No. US20030032200A1

; GENERAL INFORMATION:

; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 12
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-262

Query Match 37.5%; Score 27; DB 10; Length 12;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CASELKGK 7
Db 6 CTTTELGR 12

RESULT 15
US-09-791-389-262
; Sequence 262, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 12
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-262

Query Match 37.5%; Score 27; DB 10; Length 12;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CASELKGK 7
Db 6 CTTTELGR 12

Search completed: September 5, 2004, 10:37:18
Job time : 68 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:29:31 ; Search time 15 Seconds
(without alignments)
44.743 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 127817

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	38.9	9	3	US-09-258-754-63
2	28	38.9	9	3	US-09-042-107-63
3	28	38.9	9	4	US-09-722-250D-63
4	27	37.5	13	1	US-07-732-114A-2
5	27	37.5	13	1	US-08-170-114A-2
6	26	36.1	9	3	US-08-660-092-70
7	26	36.1	9	4	US-09-160-513-70
8	26	36.1	13	3	US-09-258-754-219
9	26	36.1	13	3	US-09-042-107-219
10	26	36.1	13	4	US-09-722-250D-219
11	26	36.1	13	4	US-09-428-082B-170
12	24.5	34.0	12	4	US-08-182-967-12
13	24	33.3	7	2	US-08-645-193B-3
14	24	33.3	9	6	5217869-110
15	24	33.3	11	3	US-08-866-545-24
16	24	33.3	11	4	US-09-428-082B-116
17	24	33.3	11	4	US-09-627-775-24
18	24	33.3	13	3	US-09-258-754-183
19	24	33.3	13	3	US-09-042-107-183
20	24	33.3	13	4	US-08-182-967-11
21	24	33.3	13	4	US-07-732-250D-183
22	23.5	32.6	11	1	US-07-732-114A-6
23	23.5	32.6	11	1	US-08-170-114A-6
24	23	31.9	7	2	US-08-645-193B-7
25	23	31.9	7	2	US-08-645-193B-59
26	23	31.9	9	3	US-08-660-092-150
27	23	31.9	9	3	US-08-660-092-151

28	23	31.9	9	3	US-08-660-092-152	Sequence 152, App
29	23	31.9	9	4	US-09-160-513-150	Sequence 150, App
30	23	31.9	9	4	US-09-160-513-151	Sequence 151, App
31	23	31.9	9	4	US-09-160-513-152	Sequence 152, App
32	23	31.9	10	1	US-08-250-789A-91	Sequence 91, Appl
33	23	31.9	10	4	US-09-489-847-344	Sequence 344, Appl
34	23	31.9	11	1	US-08-212-433A-30	Sequence 30, Appl
35	23	31.9	11	3	US-08-716-256-30	Sequence 30, Appl
36	23	31.9	11	4	US-09-069-827A-35	Sequence 35, Appl
37	23	31.9	11	5	PCT-US95-03239-30	Sequence 30, Appl
38	23	31.9	12	1	US-07-732-114A-1	Sequence 1, Appl
39	23	31.9	12	1	US-08-170-114A-1	Sequence 1, Appl
40	23	31.9	12	4	US-08-811-682-20	Sequence 20, Appl
41	23	31.9	12	4	US-09-089-878-1	Sequence 1, Appl
42	23	31.9	13	4	US-09-089-878-2	Sequence 2, Appl
43	22.5	31.2	12	4	US-09-460-384-9	Sequence 9, Appl
44	22	30.6	7	4	US-09-187-859-1066	Sequence 1066, Ap
45	22	30.6	7	4	US-09-839-542B-1066	Sequence 1066, Ap

ALIGNMENTS

RESULT 1
US-09-258-754-63
; Sequence 63, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-63

Query Match 38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTFC 13
:|||||
Db 3 RSTNTGC 9

RESULT 2
US-09-042-107-63
; Sequence 63, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9

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;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-63

Query Match          38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 KSTNTFC 13
      :|||||
Db      3 RSTNTGC 9

RESULT 3
US-09-722-250D-63
; Sequence 63, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-63

Query Match          38.9%; Score 28; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 KSTNTFC 13
      :|||||
Db      3 RSTNTGC 9

RESULT 4
US-07-732-114A-2
; Sequence 2, Application US/07732114A
; Patent No. 5298396
; GENERAL INFORMATION:
; APPLICANT: KOTZIN, BRIAN L.
; APPLICANT: MARRACK, PHILIPPA
; APPLICANT: KAPPLER, JOHN
; APPLICANT: PALLARD, XAVIER
; TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
; TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,114A
; FILING DATE: 18-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07,488,353
; FILING DATE: 2-MARCH-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07,437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Julie L. Bernard
; REGISTRATION NUMBER: 36,450
; REFERENCE/DOCKET NUMBER: NUH217.3
```

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;
; APPLICATION NUMBER: US/07/732,114A
; FILING DATE: 18-JULY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/488,353
; FILING DATE: 2-MARCH-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-07-732-114A-2

Query Match          37.5%; Score 27; DB 1; Length 13;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 CASELGKSTNT 11
      :|||
Db      1 CASSLYGTRNT 11

RESULT 5
US-08-170-114A-2
; Sequence 2, Application US/08170114A
; Patent No. 5776708
; GENERAL INFORMATION:
; APPLICANT: KOTZIN, BRIAN L.
; APPLICANT: MARRACK, PHILIPPA
; APPLICANT: KAPPLER, JOHN
; APPLICANT: PALLARD, XAVIER
; TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
; TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0 (a) For Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,114A
; FILING DATE: 20-DECEMBER-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/732,114
; FILING DATE: 18-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07,488,353
; FILING DATE: 2-MARCH-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07,437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Julie L. Bernard
; REGISTRATION NUMBER: 36,450
; REFERENCE/DOCKET NUMBER: NUH217.3
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-170-114A-2

Query Match 37.5%; Score 27; DB 1; Length 13;
Best Local Similarity 54.5%; Pred. No. 2.le+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11
DB 1 CASSLYGTRNT 11

RESULT 6

US-08-660-092-70
Sequence 70, Application US/08660092
Patent No. 6207160
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Marquis, David M.
APPLICANT: Jones, David S.
APPLICANT: Yu, Lin
TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES
TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED
TITLE OF INVENTION: PATHOLOGIES
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,092
FILING DATE: 06-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Park, Freddie K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 25231-20061.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-092-70

Query Match 36.1%; Score 26; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGK 7
DB 1 CAGVLGK 7

RESULT 7

US-09-160-513-70
Sequence 70, Application US/09160513
Patent No. 6410775
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Marquis, David M.
APPLICANT: Jones, David S.
APPLICANT: Yu, Lin
TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,513
FILING DATE: 1998-DEC-24
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 25231-20061.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-160-513-70

Query Match 36.1%; Score 26; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGK 7
DB 1 CAGVLGK 7

RESULT 8

US-09-258-754-219
Sequence 219, Application US/09258754
Patent No. 6174687
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Dipeptidase
FILE REFERENCE: P-LJ 3443
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/042,107
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 219
LENGTH: 13

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-219

Query Match      36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 7; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 9
US-09-042-107-219
; Sequence 219, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-219

Query Match      36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 7; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 10
US-09-722-250D-219
; Sequence 219, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-219

Query Match      36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 7; Gaps 0;
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QY 1 CASELGKSTNTFC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 11
US-09-428-082B-170
; Sequence 170, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CALMODULIN ANTAGONIST PEPTIDE
US-09-428-082B-170

Query Match      36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NTFC 13
Db 8 NTFC 11

RESULT 12
US-08-182-967-12
; Sequence 12, Application US/08182967
; Patent No. 6413516
; GENERAL INFORMATION:
; APPLICANT: Chang, Jennie C.C.
; APPLICANT: Brostoff, Steven W.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Peptides and Methods Against Psoriasis
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,967
; FILING DATE: 14-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,471
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,867
; FILING DATE: 14-DEC-1991
; PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 07/644,611
/ FILING DATE: 22-JAN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/530,229
/ FILING DATE: 30-MAY-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/382,085
/ FILING DATE: 18-JUL-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/382,086
/ FILING DATE: 18-JUL-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/326,314
/ FILING DATE: 21-MAR-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-IM 9830
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-182-967-12

Query Match 34.0%; Score 24.5; DB 4; Length 12;
Best Local Similarity 63.6%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
DB 1 CASSL-NSLNT 10

RESULT 13
US-08-645-193B-3
/ Sequence 3, Application US/08645193B
/ Patent No. 5962253
/ GENERAL INFORMATION:
/ APPLICANT: Kupke, Thomas
/ APPLICANT: Gotz, Friedrich
/ APPLICANT: Kempter, Christoph
/ APPLICANT: Jung, Gunther
/ TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
/ TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
/ NUMBER OF SEQUENCES: 70
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
/ STREET: 1100 New York Avenue, Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/645,193B
/ FILING DATE: 13-MAY-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Esmond, Robert W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0652.1540000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540

/ APPLICATION NUMBER: US 07/644,611
/ FILING DATE: 22-JAN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/530,229
/ FILING DATE: 30-MAY-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/382,085
/ FILING DATE: 18-JUL-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/382,086
/ FILING DATE: 18-JUL-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/326,314
/ FILING DATE: 21-MAR-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-IM 9830
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-182-967-12

Query Match 34.0%; Score 24.5; DB 4; Length 12;
Best Local Similarity 63.6%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
DB 1 CASSL-NSLNT 10

RESULT 13
US-08-645-193B-3
/ Sequence 3, Application US/08645193B
/ Patent No. 5962253
/ GENERAL INFORMATION:
/ APPLICANT: Kupke, Thomas
/ APPLICANT: Gotz, Friedrich
/ APPLICANT: Kempter, Christoph
/ APPLICANT: Jung, Gunther
/ TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
/ TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
/ NUMBER OF SEQUENCES: 70
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
/ STREET: 1100 New York Avenue, Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/645,193B
/ FILING DATE: 13-MAY-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Esmond, Robert W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0652.1540000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540

/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: peptide
/ US-08-645-193B-3

Query Match 33.3%; Score 24; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 STNTEC 13
DB 1 SFNSFC 6

RESULT 14
5217869-110
/ Patent No. 5217869
/ APPLICANT: KAUVAR, LAWRENCE M.
/ TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
/ REAGENTS
/ NUMBER OF SEQUENCES: 121
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/255,906
/ FILING DATE: 11-OCT-1988
/ SEQ ID NO: 110:
/ LENGTH: 9
/ 5217869-110

Query Match 33.3%; Score 24; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTF 12
DB 1 GKGSNNF 7

RESULT 15
US-08-866-545-24
/ Sequence 24, Application US/08866545
/ Patent No. 6265535
/ GENERAL INFORMATION:
/ APPLICANT: Greene, Mark I.
/ APPLICANT: Murali, Ramachandran
/ APPLICANT: Takasaki, Wataru
/ TITLE OF INVENTION: PEPTIDES AND PEPTIDE
/ TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
/ TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/866,545
/ FILING DATE: 30-MAY-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009113-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6265535e
US-08-866-545-24

Query Match 33.3%; Score 24; DB 3; Length 11;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELCK 7
Db 2 CRKELGQ 8

Search completed: September 5, 2004, 10:32:42
Job time : 16 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:36:12 ; Search time 22 Seconds
(without alignments)
34.979 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNERSLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 605

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	37.0	6	2 S29637	jacalin beta-II ch
2	17	37.0	6	2 I37263	Y protein - human
3	15	32.6	6	2 JU0355	lipopeptide WS1279
4	15	32.6	7	2 B39040	calsequestrin, fas
5	15	32.6	8	2 S59622	metallothionein is
6	15	32.6	8	2 S19288	acylase - Kluuyvera
7	15	32.6	8	2 S63165	ferredoxin a2 - Ja
8	14	30.4	6	2 B31263	dihydrofolate redu
9	14	30.4	6	2 S29881	Na+/K+-exchanging
10	14	30.4	7	1 XEYDGD	galactose oxidase
11	14	30.4	8	2 B47594	aspartate kinase (
12	13	28.3	5	2 A32014	tram protein - Esc
13	13	28.3	8	2 A37521	R-phycoerythrin ga
14	12	26.1	6	2 H48394	glycoprotein compo
15	12	26.1	7	2 B34818	vicilin 57K chain
16	12	26.1	7	2 A12016	formylglycinamide
17	12	26.1	8	2 PC1002	leucine-tRNA ligase
18	11	23.9	4	2 A41890	protein D - Escher
19	11	23.9	5	2 A26830	mitosis inhibiting
20	11	23.9	5	2 B25655	R-phycoerythrin al
21	11	23.9	5	2 A44692	fulicin - giant Af
22	11	23.9	6	2 A31263	dihydrofolate redu
23	11	23.9	7	2 A58512	venom heptapeptide
24	11	23.9	7	2 A46868	alpha-myosin heavy
25	11	23.9	8	2 C61512	variant surface gl
26	11	23.9	8	2 PT0554	T-cell receptor be
27	10	21.7	4	2 S55238	pallidipin - assas
28	10	21.7	5	2 A60803	neuropeptide - sea
29	10	21.7	5	2 PT0610	T-cell receptor be

ALIGNMENTS

RESULT 1

S29637 jacalin beta-II chain - Artocarpus champeden (fragment)

C:Species: Artocarpus champeden

C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998

C:Accession: S29637

R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.

Biochim. Biophys. Acta 1156, 219-222, 1993

A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD

A:Reference number: S29635; MUID:93152601; PMID:8427879

A:Accession: S29637

A:Molecule type: protein

A:Residues: 1-6 <NGO>

A:Experimental source: seed

C:Function: C:Complex: heterotetramer; two alpha and two beta chains

A:Description: seed storage protein

A:Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine

C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match 37.0%; Score 17; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEES 5
DB 1 NEQS 4

RESULT 2

I37263

Y protein - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 12-Aug-1995 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999

C:Accession: I37263

R:Waechter, G.; Habener, J.F.

Endocrinology 131, 2010-2015, 1992

A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alterna

A:Reference number: I37263; MUID:93010691; PMID:1396344

A:Accession: I37263

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816

C:Genetics:

A:Gene: CREB

Query Match 37.0%; Score 17; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SLIC 8

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Db          1 SLFC 4
|||
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
JU0355
lipopeptide WS1279 [validated] - Streptomyces willmorei
C:Species: Streptomyces willmorei
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: JU0355
R;Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A;Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial or
F;Reference number: JU0355; MUID:91300586; PMID:2070441
A;Accession: JU0355
A;Molecule type: protein
A;Residues: 1-6 <TSU>
A;Note: the structure was confirmed by synthesis
C;Keywords: blocked amino end; lipoprotein
F;1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F;1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 32.6%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2
|||
Db 1 CN 2

RESULT 4
B39040
calsequestrin, fast skeletal muscle - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C:Accession: B39040
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein
A;Reference number: A39040; MUID:91093153; PMID:1985907
A;Accession: B39040
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <CAL>
C;Keywords: phosphoprotein; skeletal muscle

Query Match 32.6%; Score 15; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEESL 6
|||
Db 2 DEEDL 6

RESULT 5
S59622
metallothionein isoform a, cadmium-binding - Ariantha arbustorum (terrestrial snail) (fra
C:Species: Ariantha arbustorum
C>Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 07-May-1999
C:Accession: S59622
R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallingier, R.
Biochem. J. 311, 951-957, 1995
A;Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothion
A;Reference number: S59621; MUID:96067616; PMID:7487956
A;Accession: S59622
A;Molecule type: protein
A;Residues: 1-8 <BER>
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 32.6%; Score 15; DB 2; Length 8;

Db          1 SLFC 4
|||
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
S19288
acylase - Kluyvera cryocrescens
C:Species: Kluyvera cryocrescens
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S19288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase from K
A;Reference number: S19288; MUID:92109664; PMID:1764029
A;Accession: S19288
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAR>

Query Match 32.6%; Score 15; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2
|||
Db 1 CN 2

RESULT 7
S69165
ferredoxin a2 - Japanese radish (fragment)
C:Species: Kaiware daikon (Japanese radish)
C>Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C:Accession: S69165
R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A;Title: Four ferredoxins from Japanese radish leaves.
A;Reference number: S69164; MUID:95168867; PMID:7864635
A;Accession: S69165
A;Molecule type: protein
A;Residues: 1-8 <ORA>
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 32.6%; Score 15; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EESLI 7
|||
Db 4 EEDIV 8

RESULT 8
B31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C:Species: Plasmodium falciparum
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: B31263
R;Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A;Reference number: A9421; MUID:89057886; PMID:2504149
A;Accession: B31263
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6 <PET>
C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 30.4%; Score 14; DB 2; Length 6;

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Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEESL 6
DB 2 NWESI 6

RESULT 9
S29881
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 19-Apr-2002
C:Accession: S29881
R:Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Brikin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases around
A:Reference number: S29881; MUID:85131201; PMID:3156136
A:Accession: S29881
A:Molecule type: protein
A:Residues: 1-6 <WAL>
A:Experimental source: kidney
C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 20.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEES 5
DB 2 CSDKT 6

RESULT 10
XEYDGD
Galactose oxidase inhibitor - fungus (Cladobotryum dendroides)
C:Species: Cladobotryum dendroides
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993
C:Accession: A01341
R:Avigad, G.; Markus, Z.
Fed. Proc. 31, 447, 1972
A:Reference number: A01341
A:Accession: A01341
A:Molecule type: protein
A:Residues: 1-7 <AVI>
C:Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, may inactivate the enzyme by binding to its prosthetic copper group.
C:Superfamily: galactose oxidase inhibitor
C:Keywords: copper

Query Match 30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEES 5
DB 4 NTES 7

RESULT 11
B47594
aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)
C:Species: Corynebacterium flavum
C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
C:Accession: B47594
R:Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.
J. Bacteriol. 175, 4096-4103, 1993
A:Title: Gene structure and expression of the Corynebacterium flavum N13 ask-asd operon.
A:Reference number: A47594; MUID:93308089; PMID:8100567
A:Accession: B47594
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA

Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEESL 6
DB 2 NWESI 6

RESULT 9
S29881
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 19-Apr-2002
C:Accession: S29881
R:Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Brikin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases around
A:Reference number: S29881; MUID:85131201; PMID:3156136
A:Accession: S29881
A:Molecule type: protein
A:Residues: 1-6 <WAL>
A:Experimental source: kidney
C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 20.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEES 5
DB 2 CSDKT 6

RESULT 10
XEYDGD
Galactose oxidase inhibitor - fungus (Cladobotryum dendroides)
C:Species: Cladobotryum dendroides
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993
C:Accession: A01341
R:Avigad, G.; Markus, Z.
Fed. Proc. 31, 447, 1972
A:Reference number: A01341
A:Accession: A01341
A:Molecule type: protein
A:Residues: 1-7 <AVI>
C:Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, may inactivate the enzyme by binding to its prosthetic copper group.
C:Superfamily: galactose oxidase inhibitor
C:Keywords: copper

Query Match 30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEES 5
DB 4 NTES 7

RESULT 11
B47594
aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)
C:Species: Corynebacterium flavum
C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
C:Accession: B47594
R:Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.
J. Bacteriol. 175, 4096-4103, 1993
A:Title: Gene structure and expression of the Corynebacterium flavum N13 ask-asd operon.
A:Reference number: A47594; MUID:93308089; PMID:8100567
A:Accession: B47594
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 1-8 <FOL>
C:Keywords: phosphotransferase

Query Match 30.4%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 RESLI 7
DB 2 BEAVL 6

RESULT 12

A32014

traM protein - Escherichia coli plasmid R100 (fragment)

C:Species: Escherichia coli

C:Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 16-Feb-1997

C:Accession: A32014

R:Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.

J. Bacteriol. 170, 2749-2757, 1988

A:Title: Identification and characterization of the products from the traJ and traY gene

A:Reference number: A32014; MUID:89227859; PMID:2836369

A:Accession: A32014

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <INA>

C:Genetics:

A:Genome: plasmid

C:Keywords: DNA binding

Query Match 28.3%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4
DB 2 NDE 4

RESULT 13

A37521

R-phycoerythrin gamma-E chain - red alga (Gastrocloonium coulteri) (fragment)

C:Species: Gastrocloonium coulteri

C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C:Accession: A37521; J22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601; PMID:3886644

A:Accession: A37521

A:Molecule type: protein

A:Residues: 1-8 <KLO>

Query Match 28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SLIC 8
DB 4 ALAC 7

RESULT 14

H48394

glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr

C:Species: Bos primigenius taurus (cattle)

C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

C:Accession: H48394

R:Mather, I.H.; Banghart, L.R.; Lane, W.S.

Biochem. Mol. Biol. Int. 29, 545-554, 1993

A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig

II-like sequences.

A:Reference number: A48394; MUID:93250576; PMID:8485470

A;Accession: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <MA>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein

Query Match 26.1%; Score 12; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ESLIC 8
DB 2 ELLGC 6

RESULT 15
B34818
vicilin 57K chain - pigeon pea (fragment)
C;Species: Cajanus cajan (pigeon pea)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C;Accession: B34818
R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A;Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A;Reference number: A34818; MUID:90165956; PMID:2306256
A;Accession: B34818
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MA>

Query Match 26.1%; Score 12; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNE 3
DB 3 CME 5

Search completed: September 5, 2004, 10:40:20
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:32:47 ; Search time 15 Seconds
(without alignments)
27.771 Million cell updates/sec

Title: US-09-761-636A-6
Perfect score: 46
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	14	30.4	7	1	IGAO_DACDE
2	13	28.3	5	1	TRM3_ECOLI
3	13	28.3	7	1	PLP_BRANA
4	12	26.1	7	1	UF03_MOUSE
5	12	26.1	8	1	UPA1_HUMAN
6	11	23.9	7	1	BRHP_CONIM
7	11	23.9	7	1	FAR1_ASCSU
8	11	23.9	8	1	CAD1_ENTFA
9	10	21.7	8	1	ACT_CARMA
10	9	19.6	6	1	TMOF_SARBU
11	9	19.6	8	1	COM2_CONPU
12	9	19.6	8	1	GLUR_HUMAN
13	8	17.4	6	1	ACPH_RABIT
14	8	17.4	6	1	ASP2_LACSN
15	8	17.4	7	1	CCF1_ENTFA
16	8	17.4	7	1	FAR1_PROCL
17	8	17.4	7	1	GRFP_MOUSE
18	8	17.4	7	1	WMA3_ACHPU
19	8	17.4	7	1	WMA3_ACHPU
20	8	17.4	8	1	FAR4_HOMAM
21	8	17.4	8	1	FAR8_CALVO
22	7	15.2	7	1	FAR2_ASCSU
23	7	15.2	7	1	UHL1_RAT
24	7	15.2	8	1	CLP_THICU
25	7	15.2	8	1	CPD1_ENTFA
26	7	15.2	8	1	PPK3_PERAM
27	7	15.2	8	1	UH03_RAT
28	7	15.2	8	1	WPI_PERAT
29	6	13.0	4	1	EOST_HUMAN
30	6	13.0	4	1	FLRN_ANTEL
31	6	13.0	5	1	TPIS_CANFA
32	6	13.0	5	1	UXA4_CHLTR
33	6	13.0	6	1	FARP_MONEX

34	6	13.0	6	1	UN06_CLOPA
35	6	13.0	6	1	VP19_HSVIK
36	6	13.0	7	1	ALL2_CARMA
37	6	13.0	7	1	ALL5_CARMA
38	6	13.0	7	1	CHOX_ALCSP
39	6	13.0	7	1	EI05_LITRU
40	6	13.0	7	1	FAR1_MACRS
41	6	13.0	7	1	FAR2_PROCL
42	6	13.0	7	1	FAR4_PANRE
43	6	13.0	7	1	FARB_CALVO
44	6	13.0	7	1	LANC_CARUI
45	6	13.0	7	1	MNP1_LEPDE

P81351	clostridium
P23210	herpes simp
P81805	carcinus ma
P81808	carcinus ma
P16101	alcaligenes
P82101	litoria rub
P83274	macrobrachi
P38498	procamburus
P41875	panagrellus
P41866	calliphora
P36960	carnobacter
P42984	leptinotars

ALIGNMENTS

RESULT 1
IGAO_DACDE STANDARD; PRT; 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
OX NCBI_TaxID=5132;
RN [1]
RP SEQUENCE.
RA Avigad G., Markus Z.;
RT "Identification of a peptide inhibitor of galactose oxidase from
RT Dactylium dendroides.";
RL Fed. Proc. 31:447-447(1972).
CC -!- FUNCTION: Binds one copper ion per molecule but does not bind the
CC galactose oxidase apoenzyme. It may inactivate the enzyme by
CC binding to its prosthetic copper group.
DR PIR; A01341; XEYDGD.
KW Copper; Metalloenzyme inhibitor.
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEES 5
Db 4 NTES 7

RESULT 2
TRM3_ECOLI STANDARD; PRT; 5 AA.
ID TRM3_ECOLI
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TrmM protein (Fragment).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traj
RT and trm genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).

CC -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION

CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- SIMILARITY: Belongs to the tram family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; M20941; -; NOT_ANNOTATED_CDS.
 CC DR PIR; A32014; A32014.
 CC KW Conjugation; Plasmid; DNA-binding.
 CC FT NON_TER 1
 CC SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;

Query Match 28.3%; Score 13; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NEE 4
 Db 2 NDE 4

RESULT 3
 PLP BRANA
 ID UPAL_HUMAN STANDARD; PRT; 8 AA.
 AC P81707;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Plastidial lipid-associated protein (Fragment).
 OS Brassica napus (Rape).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Brassicales; Brassicaceae; Brassica.
 CC NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. TOPAZ; TISSUE=Tapetum;
 RX MEDLINE=99349136; PubMed=10420651;
 RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
 RA Murphy D.J.;
 RT "Composition and role of tapetal lipid bodies in the biogenesis of the
 RT pollen coat of Brassica napus.";
 RL Planta 208:588-598(1999).
 CC -|- FUNCTION: May play a structural role in the elaioplast, a tapetum-
 CC specific plastidial lipid organelle.
 CC -|- TISSUE SPECIFICITY: Tapetum of anthers.
 CC FT NON_TER 8
 CC SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 28.3%; Score 13; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NEE 4
 Db 5 NDE 7

RESULT 4
 UF03 MOUSE
 ID UF03 MOUSE STANDARD; PRT; 7 AA.
 AC P38641;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.1, its MW is: 36 kDa.
 CC FT NON_TER 7
 CC SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DDDB1B1180 CRC64;

Query Match 26.1%; Score 12; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NEE 5
 Db 1 HEEA 4

RESULT 5
 UPAL_HUMAN
 ID UPAL_HUMAN STANDARD; PRT; 8 AA.
 AC P30087;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.9, its MW is: 65 kDa.
 CC DR SWISS-2DPAGE; P30087; HUMAN.
 CC FT NON_TER 1
 CC FT UNSURE 8
 CC FT NON_TER 8
 CC SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 26.1%; Score 12; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NEE 5
 Db 1 DQES 4

RESULT 6
 BRHP CONIM
 ID BRHP CONIM STANDARD; PRT; 7 AA.
 AC P58803;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bromheptapeptide Im.
 CC Conus imperialis (Imperial cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=35631;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=97184108; PubMed=9030520;
 RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
 RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
 RA McIntosh J.M.;
 RT "A novel post-translational modification involving bromination of
 RT tryptophan. Identification of the residue, L-6-bromotryptophan, in
 RT peptides from *Conus imperialis* and *Conus radiatus* venom.";
 RL J. Biol. Chem. 272:4689-4698(1997).
 CC -!- FUNCTION: Does not elicit gross behavioral symptoms when injected
 CC centrally or peripherally in mice.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.
 DR PIR; A58512; A58512.
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.
 FT DISULFID 2 7
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 6 6 BROMINATION.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;
 Query Match 23.9%; Score 11; DB 1; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CNE 3
 Db 2 CQ 4
 RESULT 7
 ID FAR1 ASCSU STANDARD; PRT; 7 AA.
 AC P31869;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRPamide-like neuropeptide AFI.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90180465; PubMed=2627377;
 RA Cowden C., Stretton A.O.W., Davis R.E.;
 RT "AFI, a sequenced bioactive neuropeptide isolated from the nematode
 RT *Ascaris suum*.";
 RL Neuron 2:1465-1473(1989).
 CC -!- FUNCTION: Potent modulator of inhibitory motoneurons. Reduces the
 CC input resistance and blocks slow oscillatory potentials in these
 CC cells.
 CC -!- TISSUE SPECIFICITY: Found in the nerve cords and a variety of
 CC ganglia particularly in the anterior regions.
 CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 953 MW; 69D40059CB14350 CRC64;
 Query Match 23.9%; Score 11; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NE 3
 Db 2 NE 3

RESULT 8
 CADI_ENTFA
 ID CADI_ENTFA STANDARD; PRT; 8 AA.
 AC P13268;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CADI.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85051889; PubMed=6437872;
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B., Suzuki A.;
 RT "Isolation and structure of the bacterial sex pheromone, CADI, that
 RT induces plasmid transfer in *Streptococcus faecalis*.";
 RL FEBS Lett. 178:97-100(1984).
 CC -!- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PAD1.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;
 Query Match 23.9%; Score 11; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SLI 7
 Db 3 SLV 5
 RESULT 9
 ACT_CARMA
 ID ACT_CARMA STANDARD; PRT; 8 AA.
 AC P80709;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Actin (Fragment).
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
 RA Bagdasarian D.;
 RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
 RL Endocrine 5:23-32(1996).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 6.8, ITS MW IS: 46 kDa.
 CC -!- SIMILARITY: Belongs to the actin family.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR PROSITE; PS00406; ACTINS_1; PARTIAL.
 DR PROSITE; PS00432; ACTINS_2; PARTIAL.
 DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
 KW Structural protein.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;
 Query Match 21.7%; Score 10; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2
|:
2 CD 3

RESULT 10

TMOF_SARBU ID TMOF_SARBU STANDARD; PRT; 6 AA.
AC P41435;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Ovary;
RX MEDLINE=94211930; PubMed=8159807;
RA Bylenans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
de Loof A.;
RT Sequencing and characterization of trypsin modulating oostatic
factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
RT (Sarcophaga) bullata.";
RL Regul. Pept. 50:61-72(1994).
CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
in the midgut which indirectly reduces the vitellogenin
concentration in the hemolymph resulting in inhibition of oocyte
development.
CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular
epithelium after a blood meal.
KW Hormone.
SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 19.6%; Score 9; DB 1; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NEESL 6
|:
1 NPTNL 5

RESULT 11

COM2_CONPU ID COM2_CONPU STANDARD; PRT; 8 AA.
AC F58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.

CC -1- SIMILARITY: Belongs to the contryphan family.

KW Toxin; Hydroxylation; D-amino acid.

FT DISULFID 2 8
|:
MOD RES 4 4 D-LEUCINE.

SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match

19.6%; Score 9; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|:
2 C 2

RESULT 12

GLUR_HUMAN ID GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urine glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=72062338; PubMed=5126885;

RA Lote C.J., Weiss J.B.;

RT Identification in urine of a low-molecular-weight highly polar

RT glycopeptide containing cysteinyl-galactose.";

RL Biochem. J. 123:25P-25P(1971).

CC -1- FUNCTION: The identity of the glycoprotein from which this peptide

is derived is unknown. No physiological function has been

attributed. An erythrocyte membrane glycopeptide having a

similar structure has also been found.

CC PIR: A03188; XGHUEU.

DR GO; GO:0005576; C:extracellular; NAS.

FT GLYCOPROTEIN.

FT CARBOHYD 1 1 S-LINKED (GAL. . .).

SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5B1EB1E CRC64;

Query Match

19.6%; Score 9; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|:
1 C 1

RESULT 13

ACPH_RABIT ID ACPH_RABIT STANDARD; PRT; 6 AA.
AC P251E4;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide
hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.

RX MEDLINE=92222120; PubMed=1807161;

RA Krishna R.G., Chin C.C.Q., Mold F.;

RT "N-terminal sequence analysis of N alpha-acetylated proteins after


```

RT unlocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991).
CC -!- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal
CC peptide bond of an N-acetylated peptide to generate an N-
CC acetylated amino acid and a peptide with a free N-terminus. It
CC preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to peptidase family S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Pept S9 AS.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLIATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 17.4%; Score 8; DB 1; Length 6;
Best Local Similarity 20.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EESLI 7
Db |::
2 ERQVL 6

RESULT 14
ASP2_LACSN
ID ASP2_LACSN STANDARD; PRT; 6 AA.
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CBI;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CBI.";
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match 17.4%; Score 8; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NE 3
Db |::
5 ND 6

RESULT 15
CCF1_ENTFA
ID CCF1_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]

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RP SEQUENCE
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces
RT conjugative transfer of the Streptococcus faecalis tetracycline
RT resistance plasmid, pCF10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC PIR; A30812; A30812.
DR Pheromone.
KW SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 17.4%; Score 8; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLI 7
Db |::
3 TLV 5

Search completed: September 5, 2004, 10:38:49
Job time : 16 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:35:32 ; Search time 57 Seconds
(without alignments)
44.283 Million cell updates/sec

Title: US-09-761-636A-6
Perfect score: 46
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 488

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	39.1	8	10 Q9SAY7	Q9say7 dioscorea t
2	16	34.8	7	12 Q67113	Q67113 influenzavi
3	16	34.8	7	13 Q42564	Q42564 fugu rubrip
4	14	30.4	8	4 Q81V87	Q81v87 homo sapien
5	13	28.3	7	11 Q55184	Q55184 rattus norv
6	13	28.3	8	2 Q32560	Q32560 escherichia
7	12	26.1	8	2 Q3ZE29	Q3ze29 buchnera ap
8	12	26.1	8	4 Q9BY5	Q9by5 homo sapien
9	12	26.1	8	4 Q15895	Q15895 homo sapien
10	12	26.1	8	4 Q15890	Q15890 homo sapien
11	12	26.1	8	6 Q9BF82	Q9bf82 ursus arcto
12	12	26.1	8	6 Q9BFC2	Q9bfc2 macropus eu
13	12	26.1	8	6 Q9BF90	Q9bf90 tragelaphus
14	12	26.1	8	6 Q9BFB1	Q9bfb1 echinops te
15	12	26.1	8	6 Q9BF93	Q9bf93 megaptera n
16	12	26.1	8	6 Q9BFA1	Q9bfa1 ateles fusc

17	12	26.1	8	6 Q9BF87	Q9bf87 tapirus ind
18	12	26.1	8	6 Q9BF89	Q9bf89 euphractus
19	12	26.1	8	6 Q9BF88	Q9bf88 chaetophrac
20	12	26.1	8	6 Q9BFA0	Q9bfa0 macaca mula
21	12	26.1	8	6 Q9BFA8	Q9bfa8 loxodonta a
22	12	26.1	8	6 Q9BFA9	Q9bfa9 procavia ca
23	12	26.1	8	6 Q9BF82	Q9bf82 sorex arane
24	12	26.1	8	6 Q9BF85	Q9bf85 erinaceus c
25	12	26.1	8	6 Q9BF86	Q9bf86 myrmecophag
26	12	26.1	8	6 Q9BF83	Q9bf83 condylura c
27	12	26.1	8	6 Q9BF88	Q9bf88 equus cabal
28	12	26.1	8	6 Q9BF95	Q9bf95 roussetus l
29	12	26.1	8	6 Q9BF99	Q9bf99 hyllobates c
30	12	26.1	8	6 Q9BF84	Q9bf84 panthera on
31	12	26.1	8	6 Q9BFC3	Q9bfc3 didelphis m
32	12	26.1	8	6 Q9BFA4	Q9bfa4 tupaia mino
33	12	26.1	8	6 Q9BFA2	Q9bfa2 tarsius ban
34	12	26.1	8	6 Q9BF85	Q9bf85 leopardus p
35	12	26.1	8	6 Q9BFC1	Q9bfc1 choleopus h
36	12	26.1	8	6 Q9BF89	Q9bf89 okapia john
37	12	26.1	8	6 Q9BF96	Q9bf96 pteropus gi
38	12	26.1	8	6 Q9BF80	Q9bf80 trichechus
39	12	26.1	8	6 Q9BF86	Q9bf86 felis silve
40	12	26.1	8	6 Q9BF92	Q9bf92 tursiops tr
41	12	26.1	8	6 Q9BF87	Q9bf87 tamandua te
42	12	26.1	8	6 Q9BF91	Q9bf91 hippopotamu
43	12	26.1	8	6 Q9BF84	Q9bf84 talpa alta
44	12	26.1	8	6 Q9BFC0	Q9bfc0 choleopus d
45	12	26.1	8	6 Q9BF98	Q9bf98 callimico g

ALIGNMENTS

RESULT 1

Q9SAY7 PRELIMINARY; PRT; 8 AA.

AC Q9SAY7; TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 24, Last annotation update)

DE Phosphoglucose isomerase (Fragment).

OS Dioscorea tokoro.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;

OC Dioscorea.

OX NCBI_TaxID=64475;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DT17-1;

EX MEDLINE=20279211; PubMed=10821191;

RA Terauchi K., Kahl G.;

RT "Rapid isolation of promoter sequences by TAIL-PCR: the 5'-flanking

RT regions of Pal and Pgi genes from yams (Dioscorea).";

RL Mol. Gen. Genet. 263:554-560(2000).

DR EMBL; AB016716; BAA32235.1;

DR GO; GO:0016833; F:isomerase activity; IEA.

KW isomerase.

FT NON TER

SQ SEQUENCE 8 AA; 839 MW; F7B05731B5A1ADD6 CRC64;

Query Match 39.1%; Score 18; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. le+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SLIC 8
Db 5 TLIC 8

RESULT 2

Q67113 PRELIMINARY; PRT; 7 AA.

AC Q67113;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3' end (Fragment).
 DE (Fragment).
 OS Influenzavirus A.
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses.
 OX NCBI_TaxID=197911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81001892; PubMed=7407922;
 RA Dhar R., Chanock R.M., Lai C.-J.;
 RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza viral mRNA deduced from cloned complete genomic sequences.";
 RL Cell 21:495-500(1980).
 DR EMBL; M25045; AAA43202.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;
 Query Match 34.8%; Score 16; DB 12; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 1;
 QY 1 CNEESLIC 8
 DB |||||
 3 CN-----IC 6
 RESULT 3
 O42564 PRELIMINARY; PRT; 7 AA.
 ID O42564;
 AC O42564;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
 GN SCN8A.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97442476; PubMed=9295353;
 RA Plummer N.W., McBurney M.W., Meisler M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
 RL J. Biol. Chem. 272:24008-24015(1997).
 DR EMBL; U97673; AAB80916.1; -.
 KW Ionic channel.
 FT NON TER 1 1
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
 Query Match 34.8%; Score 16; DB 13; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 LIC 8
 DB |||||
 3 LVC 5
 RESULT 4
 Q81V87 PRELIMINARY; PRT; 8 AA.
 ID Q81V87;
 AC Q81V87;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE DJ107712.2 (Serine palmitoyltransferase, long chain base subunit 2-like (Aminotransferase 2), variant 1) (Fragment).
 GN SPTLC2L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith M.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL050320; CAD54807.1; -.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 908 MW; 8E533682CEBEB042 CRC64;
 Query Match 30.4%; Score 14; DB 4; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 LIC 8
 DB |||||
 1 VIC 3
 RESULT 5
 O55184 PRELIMINARY; PRT; 7 AA.
 ID O55184;
 AC O55184;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Orphan receptor TR4-NS (fragment).
 GN TR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley;
 RC MEDLINE=96198747; PubMed=8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RA Detera-Wadleigh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal domain.";
 RL Endocrinology 137:1562-1571(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96299786; PubMed=8661150;
 RA Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
 RT "New variants of the human and rat nuclear hormone receptor, TR4: expression and chromosomal localization of the human gene.";
 RL Genomics 35:361-366(1996).
 DR EMBL; U59454; AAB91433.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON TER 1 1
 SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;
 Query Match 28.3%; Score 13; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 IC 8
 DB |||||
 2 IC 3

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RESULT 6
O32560
ID O32560 PRELIMINARY; PRT; 8 AA.
AC O32560;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Propionate kinase (Fragment).
GN TDCD.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=W3110;
RX MEDLINE=99449059; PubMed=10520749;
RA Hessler C., Sowers G.;
RT "The tdcE gene in Escherichia coli W3110 is separated from the rest of
RT the tdc operon by insertion of IS5 elements.";
RL DNA Seq. 9:183-188(1998).
DR EMBL; AJ001620; CAA04875.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IC 8
Db 5 IC 6

RESULT 7
O9ZEZ9 PRELIMINARY; PRT; 8 AA.
ID O9ZEZ9;
AC O9ZEZ9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
GN LEUA.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99028904; PubMed=9812361;
RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT "Structure and evolution of the leucine plasmids carried by the
RT endosymbiont (Buchnera aphidicola) from aphids of the family
RT Aphididae.";
RL FEMS Microbiol. Lett. 168:43-49(1998).
DR EMBL; AJ006874; CAA07290.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0003852; F:2-isopropylmalate synthase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Plasmid.
FT NON_TER 8
SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;

Query Match 26.1%; Score 12; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 NEESLI 7
Db 2 NSQVII 7

```

```

RESULT 8
Q9BYV5 PRELIMINARY; PRT; 8 AA.
ID Q9BYV5;
AC Q9BYV5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011664; AAG47575.1; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003677; F:DNA binding; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
Db 2 LVC 4

RESULT 9
Q15895 PRELIMINARY; PRT; 8 AA.
ID Q15895;
AC Q15895;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE (Clone XP6A10A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32075; AAA73885.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 26.1%; Score 12; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ESLI 7
Db 5 KSLV 8

```

```

RESULT 10
Q15890 ID Q15890 PRELIMINARY; PRT; 8 AA.
AC Q15890;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE (Clone Xp19G12A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindeay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32083; AAA73880.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 26.1%; Score 12; DB 4; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNE 3
Db |::
4 CSQ 6

RESULT 11
Q9BF82 ID Q9BF82 PRELIMINARY; PRT; 8 AA.
AC Q9BF82;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Ursus arctos (Brown bear) (Grizzly bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9644;
RN [1]_TaxID=9644;
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011683; AAG47591.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 6 LIC 8
Db |::
2 LYC 4

RESULT 12
Q9BFC2 ID Q9BFC2 PRELIMINARY; PRT; 8 AA.
AC Q9BFC2;
DT 01-JUN-2001 (Tremblrel. 17, Created)

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DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]_TaxID=9315;
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011621; AAG47536.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
Db |::
2 LYC 4

RESULT 13
Q9BF90 ID Q9BF90 PRELIMINARY; PRT; 8 AA.
AC Q9BF90;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Tragelaphus eurycerus (Bongo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Tragelaphus.
OX NCBI_TaxID=69297;
RN [1]_TaxID=69297;
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011673; AAG47583.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
Db |::
2 LYC 4

RESULT 14
Q9BF81 ID Q9BF81 PRELIMINARY; PRT; 8 AA.
AC Q9BF81;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Echinops telfairi (Lesser hedgehog tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinops.
 OX NCBI_TaxID=9371;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21082082; PubMed=11214319;
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals.";
 RL Nature 409:614-618(2001).
 DR EMBL; AY011632; AAG47547.1; -.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
 Db | |
 2 LYC 4

RESULT 15

Q9BF93 PRELIMINARY; PRT; 8 AA.
 AC Q9BF93;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CAMP responsive element moderator (Fragment).
 GN CREW.
 OS Megaptera novaeangliae (Humpback whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Megaptera.
 OX NCBI_TaxID=9773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082082; PubMed=11214319;
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals.";
 RL Nature 409:614-618(2001).
 DR EMBL; AY011669; AAG47580.1; -.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 1025 MW; DF02C3240EAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
 Db | |
 2 LYC 4

Search completed: September 5, 2004, 10:39:53
 Job time : 58 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:32:27 ; Search time 63 Seconds
(without alignments)
35.879 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 122046

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	8	AAU04525	AAU04525 VEGF base
2	43	93.5	8	AAU04539	AAU04539 VEGF base
3	42	91.3	8	AAU04541	AAU04541 VEGF base
4	41	89.1	8	AAU04538	AAU04538 VEGF base
5	39	84.8	8	AAU04540	AAU04540 VEGF base
6	30	65.2	8	AAU04542	AAU04542 VEGF base
7	30	65.2	8	AAU04544	AAU04544 VEGF base
8	26	56.5	8	AAU04546	AAU04546 VEGF base
9	26	56.5	8	AAU04548	AAU04548 VEGF base
10	26	56.5	8	AAU04550	AAU04550 VEGF base
11	26	56.5	8	AAU04552	AAU04552 VEGF base
12	25	54.3	8	AAU04554	AAU04554 VEGF base
13	25	54.3	8	AAU04556	AAU04556 VEGF base
14	25	54.3	8	AAU04558	AAU04558 VEGF base
15	25	54.3	8	AAU04560	AAU04560 VEGF base
16	24	52.2	8	AAU04562	AAU04562 VEGF base
17	23	50.0	8	AAU04564	AAU04564 VEGF base
18	23	50.0	8	AAU04566	AAU04566 VEGF base
19	23	50.0	8	AAU04568	AAU04568 VEGF base
20	23	50.0	8	AAU04570	AAU04570 VEGF base
21	23	50.0	8	AAU04572	AAU04572 VEGF base
22	23	50.0	8	AAU04574	AAU04574 VEGF base
23	23	50.0	8	AAU04576	AAU04576 VEGF base
24	23	50.0	8	AAU04578	AAU04578 VEGF base
25	23	50.0	8	AAU04580	AAU04580 VEGF base

26	23	50.0	8	AAE08176	AAE08176 Peptide #
27	23	50.0	8	AAE08175	AAE08175 Peptide #
28	23	50.0	8	ABG34995	ABG34995 Human pro
29	23	50.0	8	ABG34987	ABG34987 Human pro
30	23	50.0	8	AAU81097	AAU81097 Integrin
31	23	50.0	8	ABU72952	ABU72952 Integrin
32	22	47.8	6	AAE93979	AAE93979 Partial p
33	22	47.8	6	AAE93979	AAE93979 Partial p
34	22	47.8	6	AAE93979	AAE93979 Partial p
35	22	47.8	7	AAE93979	AAE93979 Partial p
36	22	47.8	8	AAE93979	AAE93979 Partial p
37	22	47.8	8	AAE93979	AAE93979 Partial p
38	22	47.8	8	AAE93979	AAE93979 Partial p
39	22	47.8	8	AAE93979	AAE93979 Partial p
40	22	47.8	8	AAE93979	AAE93979 Partial p
41	22	47.8	8	AAE93979	AAE93979 Partial p
42	21	45.7	5	AAE93979	AAE93979 Partial p
43	21	45.7	5	AAE93979	AAE93979 Partial p
44	21	45.7	6	AAE93979	AAE93979 Partial p
45	21	45.7	6	AAE93979	AAE93979 Partial p

ALIGNMENTS

RESULT 1
AAU04525
ID AAU04525 standard; peptide; 8 AA.
XX AC AAU04525;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 2.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..8
FT Note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
XX WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclising a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation, diabetes induced neovascular
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 46; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 |||||
 Db 1 CNEESLIC 8

RESULT 2
 AAU04539
 ID AAU04539 standard; peptide; 8 AA.

XX AC AAU04539;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based monocyclic peptide 17.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Disulfide-bond 1. .8

FT /note= "This bond cyclises the peptide"

XX PN WO200152875-A1.

XX PD 26-JUL-2001.

XX PF 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176293P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX XX (LUDW-) LUDWIG INST CANCER RES.

XX XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX XX WPI; 2001-442248/47.

XX DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 XX from an exposed loop of a growth factor protein by oxidizing the cysteine
 XX

PT residues.

XX Example 25; Page 47; 102pp; English.

XX CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 8 AA;

Query Match 93.5%; Score 43; DB 4; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.4e+06;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 |||||
 Db 1 CNEETLIC 8

RESULT 3

AAU04541

ID AAU04541 standard; peptide; 8 AA.

XX AC AAU04541;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based monocyclic peptide 19.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Disulfide-bond 1. .8

FT /note= "This bond cyclises the peptide"

XX PN WO200152875-A1.

XX PD 26-JUL-2001.

XX PF 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176293P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX XX

PA (LUDW-) LUDWIG INST CANCER RES.
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 DR
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 25; Page 47; 102pp; English.
 PS
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 XX SQ Sequence 8 AA;
 Query Match 91.3%; Score 42; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 |||||:
 Db 1 CNEESVVC 8
 RESULT 4
 AAU04538
 ID AAU04538 standard; peptide; 8 AA.
 XX
 AC AAU04538;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 DE VEGF based monocyclic peptide 16.
 XX
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..8
 FT /note= "This bond cyclises the peptide"
 XX

PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293p.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 PI WPI; 2001-442248/47.
 DR
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 25; Page 47; 102pp; English.
 PS
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 XX SQ Sequence 8 AA;
 Query Match 89.1%; Score 41; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 |||||:
 Db 1 CNEESLIC 8
 RESULT 5
 AAU04540
 ID AAU04540 standard; peptide; 8 AA.
 XX
 AC AAU04540;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 DE VEGF based monocyclic peptide 18.
 XX
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers
 XX Disulfide-bond 1..8
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 from an exposed loop of a growth factor protein by oxidizing the cysteine
 residues.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 whose 3-dimensional structure is modelled on the exposed loop of human
 VEGF (vascular endothelial growth factor). The invention relates to a
 method of producing a monomeric monocyclic peptide by a measuring beta-
 beta carbon separation distances on opposite antiparallel strands of a
 peptide loop fragment from an exposed loop of a growth factor protein and
 cyclising the peptide by oxidising the cysteine residues. The monocyclic
 peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 peptides) and a cyclic peptide with at least one amino acid deleted prior
 to cyclisation are used to interfere with angiogenesis,
 neovascularisation or lymphangiogenesis in a mammal with a condition
 characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 The condition is diabetic retinopathy, psoriasis, arthropathy,
 hemangioma, vascularised malignant or benign tumour, post-recovery
 cerebrovascular accident, post-angioplasty stenosis, head, heat or cold
 trauma, substance-induced neovascularisation of the liver, excessive
 hormone-related angiogenic dysfunction, diabetes induced neovascular
 sequelae, hypertension induced neovascular sequelae, or chronic liver
 infection. The peptides are also used to modulate vascular permeability
 in a mammal (the mammal has a condition characterised by fluid
 accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 or brain). The peptides are used to image blood vessels and lymphatic
 vasculature. The monomeric and bicyclic peptides are used to interfere
 with at least one biological activity induced by VEGF, VEGF-C or -D and
 are also used in combination with an anti-inflammatory agent, to treat a
 chronic inflammation, especially rheumatoid arthritis, psoriasis and
 diabetic retinopathy

XX Sequence 8 AA;

Query Match 84.8%; Score 39; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 |||:|
 Db 1 CNEESPIC 8

RESULT 6

AAR24954

ID AAR24954 standard; protein; 8 AA.

XX AAR24954;
 XX 25-MAR-2003 (revised)
 DT 04-DEC-1992 (first entry)
 XX Conformationally constrained HIV inhibitory peptide.
 XX Human immunodeficiency virus; AIDS; envelope glycoproteins; CD4;
 KW cell surface protein; infection.
 XX Synthetic.

XX Key Location/Qualifiers
 XX Disulfide-bond 1..8
 FT /note= "conformationally constraining gp."
 FT Peptide 3..6
 FT /note= "beta-turn or beta-turn mimic tetrapeptide"
 FT Region 7..8
 FT /note= "conformationally constraining gp."

XX WO9209625-A1.

XX 11-JUN-1992.

XX 27-NOV-1991; 91WO-US008873.

XX 29-NOV-1990; 90US-00619782.

XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (UYCO) UNIV COLUMBIA NEW YORK.

XX Bhatnagar PK, Jarlais RLD, Dixon JS, Hendrickson WA, Kopple KD;
 PI Kwong P, Peishoff CE, Ryu SE, Truneh A, Sweet RW;

XX WPI; 1992-217018/26.

XX Conformationally constrained peptides used for inhibiting HIV - by
 mimicking the stereochemical regions of the CD4 receptor protein.

XX Example; Page 24; 37pp; English.

XX The peptide is conformationally constrained by groups attached to each
 side. The peptide mimics a beta turn and can bind to at least one HIV
 envelope protein, thus inhibiting infection. It inhibits the interaction
 between HIV envelope glycoproteins and human cell-surface protein CD4 by
 mimicking structures of CD4. See also AAR24950-R24959 and AAR25122.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 8 AA;

Query Match 65.2%; Score 30; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 |||:|
 Db 1 CMQGSFLC 8

RESULT 7

AAY54526

ID AAY54526 standard; peptide; 8 AA.

XX AAY54526;

XX 25-APR-2000 (first entry)

XX Human CD4 protein target antigenic peptide pl615.

XX Human; CD4 protein; antigenic peptide; CD4-like domain; apoptosis;
 KW syncytia formation; human immune deficiency virus; HIV binding;

KW CD4-Class II interaction; immunisation; CD4 surface complex;
 KW immune response; transplant rejection; autoimmune disease; cyclic;
 KW rheumatoid arthritis; systemic lupus erythematosus; psoriasis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..8
 FT /note= "this peptide is conformationally restricted by
 FT cyclisation"
 XX
 FN WO9967294-A1.
 XX
 XX 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US014030.
 XX
 PR 20-JUN-1998; 98US-00100409.
 XX
 FA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI; 2000-160579/14.
 XX
 PT New antigenic peptide from the CDR2 domain of CD4, for immunization
 PT against e.g. human immune deficiency virus.
 XX
 PS Disclosure; Page 63; 106pp; English.
 XX
 CC The present sequence represents a target antigenic peptide derived from
 CC the CDR2-like domain of the human CD4 protein. The peptide is cyclised by
 CC the addition of cysteine residues at either end. The specification
 CC describes antigenic peptides derived from the CDR2-like domain of CD4
 CC (amino acids 27-66 of AAR73500). These antigenic peptides present
 CC neutralising receptor/co-receptor effector sites of the CDR2-like domain.
 CC The peptides evoke effective antibody responses by having optimised site-
 CC specificity. The induced antibodies block human immune deficiency virus
 CC (HIV) binding and syncytia formation. They may also block CD4-Class II
 CC interactions with other cells, deliver signals to T cells (inhibiting
 CC normal CD4+-mediated immunoregulatory functions) or induce apoptosis of
 CC CD4 cells by simultaneous engagement of T cell receptors. Conjugates and
 CC peptides containing the antigenic peptides are used for active
 CC immunisation to generate antibodies against CD4 surface complexes,
 CC especially to prevent binding of HIV to CD4 and thus HIV infection, but
 CC also to treat undesirable immune responses such as transplant rejection,
 CC or autoimmune diseases (rheumatoid arthritis, systemic lupus
 CC erythematosus or psoriasis). These conjugates produce high-titre
 CC antibodies which are broadly neutralising against primary isolates from
 CC all classes of HIV-1 and of HIV-2. The peptides may include a promiscuous
 CC T helper epitope that is active in genetically diverse subjects
 XX
 SQ Sequence 8 AA;
 Query Match 65.2%; Score 30; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CNESSLIC 8
 Db 1 CNOGSFLC 8
 RESULT 8
 AAR73351
 ID AAR73351 standard; peptide; 8 AA.
 XX
 AC AAR73351;
 XX
 DT 12-DEC-1995 (first entry)
 XX
 XX Human TSH receptor (residues 301-308).

XX
 KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
 KW affinity; detection.
 XX
 OS Synthetic.
 XX
 PN JP07089991-A.
 XX
 PD 04-APR-1995.
 XX
 PF 28-SEP-1993; 93JP-00240853.
 XX
 PR 28-SEP-1993; 93JP-00240853.
 XX
 XX (MITP) MITSUBISHI PETROCHEMICAL CO LTD.
 XX
 DR WPI; 1995-167251/22.
 XX
 PT Novel polypeptide(s) having affinity for the human TSH receptor antibody
 PT - used in detection of the TSH antibody.
 XX
 PS Example 1; Page 25; 54pp; Japanese.
 XX
 CC Peptides with affinity to human TSH (thyroid stimulating hormone)
 CC receptor antibody are used for detection of the antibody. (See also
 CC AAR73201-592)
 XX
 SQ Sequence 8 AA;
 Query Match 56.5%; Score 26; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CNESSL 6
 Db 1 CNESSM 6
 RESULT 9
 AAR73350
 ID AAR73350 standard; peptide; 8 AA.
 XX
 AC AAR73350;
 XX
 DT 12-DEC-1995 (first entry)
 XX
 DE Human TSH receptor (residues 291-298).
 XX
 KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
 KW affinity; detection.
 XX
 OS Synthetic.
 XX
 PN JP07089991-A.
 XX
 PD 04-APR-1995.
 XX
 PF 28-SEP-1993; 93JP-00240853.
 XX
 PR 28-SEP-1993; 93JP-00240853.
 XX
 XX (MITP) MITSUBISHI PETROCHEMICAL CO LTD.
 XX
 DR WPI; 1995-167251/22.
 XX
 PT Novel polypeptide(s) having affinity for the human TSH receptor antibody
 PT - used in detection of the TSH antibody.
 XX
 PS Example 1; Page 25; 54pp; Japanese.
 XX
 CC Peptides with affinity to human TSH (thyroid stimulating hormone)
 CC receptor antibody are used for detection of the antibody. (See also
 CC AAR73201-592)
 CC

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XX      SQ      Sequence 8 AA;
Query Match          56.5%; Score 26; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 CNEESL 6
DB      3 CNESSM 8

RESULT 10
AA57040
ID      AAY57040 standard; peptide; 8 AA.
XX      AC
XX      AAY57040;
XX      DT      21-FEB-2000 (first entry)
XX      DE      Feline immunodeficiency virus immunogenic fragment.
XX      KW      Feline immunodeficiency virus; FIV; infection; diagnosis; gp130; p55;
XX      KW      immunogenic fragment; antibody; env precursor; gag precursor; cat;
XX      KW      antibody binding composition.
XX      OS      Feline immunodeficiency virus.
XX      PN      EP962774-A1.
XX      PD      08-DEC-1999.
XX      PF      14-MAY-1999; 99EP-00303760.
XX      PR      15-MAY-1998; 98US-0085615P.
XX      PR      03-JUN-1998; 98US-00089878.
XX      PA      (IDEX-) IDEXX LAB INC.
XX      PI      Groat RG, Mermer B, O'connor TP;
XX      DR      WPI; 2000-025671/03.
XX      PT      Diagnosing Feline Immunodeficiency Virus infection.
XX      PS      Disclosure; Page 4; 15pp; English.
XX      CC      This sequence is an immunogenic fragment of feline immunodeficiency virus
XX      CC      (FIV) glycoprotein 130. Peptides AAY57038-Y57039 (also fragments of
XX      CC      gp130) are used in the invention as capture polypeptides when diagnosing
XX      CC      FIV infection. The invention relates to an antibody binding composition
XX      CC      which consists of an enhanced capture polypeptide, which contains an
XX      CC      immunogenic fragment of FIV gag precursor p55, and a second fragment
XX      CC      which is part of the env precursor gp130, and an antibody-binding
XX      CC      detection composition. The invention also includes a device for
XX      CC      performing an assay which determines whether a feline is infected with
XX      CC      FIV. The novel method is used for the diagnosis of Feline
XX      CC      Immunodeficiency Virus infection
XX      SQ      Sequence 8 AA;
Query Match          56.5%; Score 26; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY      1 CNEESLIC 8
DB      1 CNQNPFFC 8

RESULT 11
AAU08451
ID      AAU08451 standard; peptide; 8 AA.
XX      AC
XX      AAU08451;
XX      DT      21-NOV-2001 (first entry)
XX      DE      Peptide A6 encoded by human VEGF-A forward primer A6-F.
XX      KW      Human; vascular endothelial growth factor; VEGF-A; vasculogenesis;
XX      KW      angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
XX      KW      age-related macular degeneration; rheumatoid arthritis; cardiovascular;
XX      KW      primer; mutant; mutein.
XX      OS      Homo sapiens.
XX      OS      Synthetic.
XX      PN      WO200162942-A2.
XX      PD      30-AUG-2001.
XX      PF      26-FEB-2001; 2001WO-US0061113.
XX      PR      25-FEB-2000; 2000US-0185205P.
XX      PR      18-MAY-2000; 2000US-0205331P.
XX      PA      (LUDW-) LUDWIG INST CANCER RES.
XX      PA      (LICN) LICENTIA OY.
XX      PI      Alitalo K, Jeltsch MM;
XX      DR      WPI; 2001-536640/59.
XX      DR      N-PSDB; AAS12807.
XX      PT      Polypeptides that bind cellular receptors for vascular endothelial growth
XX      PT      factors, polynucleotides encoding them.
XX      PS      Claim 9; Fig 7C; 261pp; English.
XX      CC      The present invention relates to polypeptides that bind cellular
XX      CC      receptors for vascular endothelial growth factors (VEGFs), the
XX      CC      polynucleotides encoding them, and their use for identifying agents that
XX      CC      modulate interactions between VEGFs and their receptors. VEGFs and their
XX      CC      receptors play an important role in vasculogenesis, the development of
XX      CC      the embryonic vasculature from early differentiating endothelial cells
XX      CC      and angiogenesis, the process of forming new blood vessels from pre-
XX      CC      existing ones. Modulators of interactions between VEGF and its receptors
XX      CC      may be used to treat dysfunction of the endothelial cell regulatory
XX      CC      system. Such disorders include cancers, abnormal angiogenesis,
XX      CC      proliferative retinopathies, age-related macular degeneration, rheumatoid
XX      CC      arthritis and psoriasis. The polypeptides of the invention exhibit unique
XX      CC      receptor binding profiles compared to known naturally occurring VEGFs.
XX      CC      AAU08446-AAU08454 represent the peptides A1-A9 which are encoded by human
XX      CC      VEGF-A forward primers used in the methods of the present invention
XX      SQ      Sequence 8 AA;
Query Match          56.5%; Score 26; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 CNEESL 6
DB      3 CNDLGL 8

RESULT 12
AAR80365
ID      AAR80365 standard; peptide; 8 AA.
XX      AC
XX      AAR80365;
XX      DT      19-APR-1996 (first entry)
XX      DE      Protein polymeric adhesion substrate glutamine donor peptide #15.

```

XX KW Pendant group; repeating unit; enzyme recognition site; sealant; fibrin;
 XX KW enzymatic cross-linking; biocompatible material; structural integrity;
 XX KW medical adhesive; wound closure; tissue repair; transglutaminase;
 XX KW protein polymer adhesive substrate.
 XX OS Synthetic.
 XX PN WO9523611-A1.
 XX PD 08-SEP-1995.
 XX PF 03-MAR-1995; 95WO-US002728.
 XX PR 03-MAR-1994; 94US-00205518.
 XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 XX PI Cappello J;
 XX DR WPI; 1995-320413/41.
 XX PT Protein polymers comprising repeating units and sequences - capable of
 PT enzyme-catalysed covalent bond formation useful as a biocompatible
 PT material for wound closure and tissue repair.
 XX PS Example 9; Page 75; 138pp; English.
 XX CC The peptides AAR80351-70 are examples of glutamine donor peptides which
 CC can be used to generate protein polymeric adhesion substrate (PPAS)
 CC conrg. repeats of non-fibrin cross-linking donor peptide sequences (see
 CC AAR80345-50 for examples of PPAS proteins). The PPAS proteins can be used
 CC as substrates in enzymatic cross-linking reactions catalysed by a
 CC transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be
 CC used in biological systems where in situ formation of a biocompatible
 CC material with structural integrity is required e.g. as medical adhesives
 CC and sealants or for wound closure or tissue repair
 XX SQ Sequence 8 AA;

Query Match 54.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 | : : :
 Db 1 CGQSKVIC 8

RESULT 13
 AAW49750
 ID AAW49750 standard; peptide; 8 AA.
 AC AAW49750;
 XX 25-MAR-2003 (revised)
 DT 12-OCT-1998 (first entry)
 XX Glutamine donor peptide.
 DE Protein polymer; adhesive sealant; wound healing; cross-linking.
 KW Synthetic.
 OS US5773577-A.
 XX 30-JUN-1998.
 XX 02-MAR-1995; 95US-00397633.
 XX 03-MAR-1994; 94US-00205518.
 XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 54.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 | : : :
 Db 1 CGQSKVIC 8

RESULT 14
 AAY48644
 ID AAY48644 standard; peptide; 8 AA.
 AC AAY48644;
 XX 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX Membrane dipeptidase-binding lung homing peptide #15.
 DE Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9946284-A2.
 XX 16-SEP-1999.
 XX 10-MAR-1999; 99WO-US005284.
 XX 13-MAR-1998; 98US-00042107.
 XX 26-FEB-1999; 99US-00258754.
 XX (BURN-) BURNHAM INST.
 XX Rajotte D, Pasqualini R, Ruoslahti EI;
 XX WPI; 1999-571717/48.
 XX New peptides which selectively home to organs or tissues, used for, e.g.
 XX identifying target ligands and for therapy of pathological conditions.
 XX Example 6; Page 144; 193pp; English.

Query Match 54.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 | : : :
 Db 1 CGQSKVIC 8

RESULT 14
 AAY48644
 ID AAY48644 standard; peptide; 8 AA.
 AC AAY48644;
 XX 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX Membrane dipeptidase-binding lung homing peptide #15.
 DE Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9946284-A2.
 XX 16-SEP-1999.
 XX 10-MAR-1999; 99WO-US005284.
 XX 13-MAR-1998; 98US-00042107.
 XX 26-FEB-1999; 99US-00258754.
 XX (BURN-) BURNHAM INST.
 XX Rajotte D, Pasqualini R, Ruoslahti EI;
 XX WPI; 1999-571717/48.
 XX New peptides which selectively home to organs or tissues, used for, e.g.
 XX identifying target ligands and for therapy of pathological conditions.
 XX Example 6; Page 144; 193pp; English.

Query Match 54.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 | : : :
 Db 1 CGQSKVIC 8

RESULT 14
 AAY48644
 ID AAY48644 standard; peptide; 8 AA.
 AC AAY48644;
 XX 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX Membrane dipeptidase-binding lung homing peptide #15.
 DE Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9946284-A2.
 XX 16-SEP-1999.
 XX 10-MAR-1999; 99WO-US005284.
 XX 13-MAR-1998; 98US-00042107.
 XX 26-FEB-1999; 99US-00258754.
 XX (BURN-) BURNHAM INST.
 XX Rajotte D, Pasqualini R, Ruoslahti EI;
 XX WPI; 1999-571717/48.
 XX New peptides which selectively home to organs or tissues, used for, e.g.
 XX identifying target ligands and for therapy of pathological conditions.
 XX Example 6; Page 144; 193pp; English.

CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue, for identifying a target molecule expressed by an organ or tissue
 CC or for treating an organ or tissue pathology, where the organ or tissue
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
 CC dipeptidase (MDP) RAY49618 to AAY49066 represent sequences which are
 CC used in the exemplification of the present invention. (Updated on 20-MAR-
 CC 2003 to correct PR field.)
 CC
 XX

SQ Sequence 8 AA;

Query Match 54.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 | | | |
 Db 1 CGNETLRC 8

RESULT 15

ABG35021
 ID ABG35021 standard; peptide; 8 AA.

XX AC ABG35021;

XX DT 15-JUL-2002 (first entry)

DE Endostatin targeting peptide #20.

XX Targeting peptide; cancer; Hodgkin's disease; cytostatic;
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
 KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
 KW inflammatory disease; arthritis; atherosclerosis; cancer;
 KW autoimmune disease; bacterial infection; viral infection.

XX OS Unidentified.

XX FN WO200220722-A2.

XX PD 14-MAR-2002.

XX PF 07-SEP-2001; 2001WO-US027702.

XX PR 08-SEP-2000; 2000US-0231266P.

XX PR 17-JAN-2001; 2001US-00765101.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Arap W, Pasqualini R;

XX DR WPI; 2002-383050/41.

XX Identifying targeting peptides useful for treating e.g. diabetes
 PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
 PT comprises exposing a sample to a phage display library and recovering
 PT phage bound to the sample.

XX Claim 56; Page 242; 298pp; English.

XX This invention relates to a novel method for identifying disease
 CC targeting peptides. The method comprises exposing a sample from an organ,
 CC tissue or cell type of interest, to a phage display library and
 CC recovering phage bound to the sample (the phage expresses targeting
 CC peptides). The peptides identified by the method of the invention may
 CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
 CC antiatherosclerotic, antidiabetic, antibacterial and antiviral
 CC activities. The methods and composition are useful for identifying
 CC targeting peptides and one or more receptors for a targeting peptide. The
 CC targeting peptides are used for selective delivery of therapeutic agents,
 CC including gene therapy vectors and fusion proteins, to specific organs,
 CC tissues, or cell types in subject. The targeting peptide may also be used

CC for treating diseases such as diabetes mellitus, inflammatory diseases,
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
 CC viral infections and Hodgkin's disease. The present sequence represents a
 CC targeting peptide of the invention

XX Sequence 8 AA;

Query Match 54.3%; Score 25; DB 5; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 | | | |
 Db 1 CSRSSFLC 8

Search completed: September 5, 2004, 10:38:28
 Job time : 65 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:38:54 ; Search time 67 Seconds
(without alignments)
37.620 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 68225

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/ECTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	8	9 US-09-761-636A-6	Sequence 6, Appli
2	43	93.5	8	9 US-09-761-636A-20	Sequence 20, Appl
3	42	91.3	8	9 US-09-761-636A-22	Sequence 22, Appl
4	41	89.1	8	9 US-09-761-636A-19	Sequence 19, Appl
5	39	84.8	8	9 US-09-761-636A-21	Sequence 21, Appl
6	26	56.5	8	9 US-09-795-006A-133	Sequence 133, App
7	25	54.3	8	12 US-10-363-208-108	Sequence 108, App
8	24	52.2	8	9 US-09-795-006A-142	Sequence 142, App
9	23	50.0	7	10 US-09-827-345-14	Sequence 14, Appl
10	23	50.0	8	9 US-09-840-277-25	Sequence 25, Appl
11	23	50.0	8	9 US-09-185-908-115	Sequence 115, App
12	23	50.0	8	12 US-10-609-217-457	Sequence 457, App
13	23	50.0	8	12 US-10-363-208-74	Sequence 74, Appl
14	23	50.0	8	12 US-10-363-208-82	Sequence 82, Appl
15	23	50.0	8	12 US-10-632-388-457	Sequence 457, App

16	23	50.0	8	12	US-10-651-723-457	Sequence 457, App
17	23	50.0	8	12	US-10-645-761-457	Sequence 457, App
18	23	50.0	8	16	US-10-666-636-457	Sequence 457, App
19	23	50.0	8	16	US-10-653-048-457	Sequence 457, App
20	22	47.8	6	14	US-10-006-869-3664	Sequence 3664, App
21	22	47.8	6	15	US-10-395-032-3664	Sequence 3664, App
22	22	47.8	7	14	US-10-006-869-3665	Sequence 3665, App
23	22	47.8	7	14	US-10-190-082-92	Sequence 92, Appl
24	22	47.8	7	15	US-10-395-032-3665	Sequence 3665, App
25	22	47.8	8	14	US-10-006-869-1071	Sequence 1071, App
26	22	47.8	8	14	US-10-006-869-3624	Sequence 3624, App
27	22	47.8	8	15	US-10-395-032-1071	Sequence 1071, App
28	22	47.8	8	15	US-10-395-032-3624	Sequence 3624, App
29	21	45.7	5	14	US-10-006-869-3663	Sequence 3663, App
30	21	45.7	5	15	US-10-395-032-3663	Sequence 3663, App
31	21	45.7	6	14	US-10-006-869-985	Sequence 985, App
32	21	45.7	6	14	US-10-006-869-2242	Sequence 2242, App
33	21	45.7	6	15	US-10-395-032-985	Sequence 985, App
34	21	45.7	6	15	US-10-395-032-2242	Sequence 2242, App
35	21	45.7	7	14	US-10-006-869-989	Sequence 989, App
36	21	45.7	7	15	US-10-006-869-2246	Sequence 2246, App
37	21	45.7	7	15	US-10-395-032-989	Sequence 989, App
38	21	45.7	7	15	US-10-395-032-2246	Sequence 2246, App
39	21	45.7	8	9	US-09-185-908-221	Sequence 221, App
40	21	45.7	8	12	US-10-363-208-77	Sequence 77, Appl
41	21	45.7	8	13	US-10-012-756-36	Sequence 36, Appl
42	21	45.7	8	14	US-10-094-401-175	Sequence 175, App
43	21	45.7	8	14	US-10-140-164-9	Sequence 9, Appli
44	21	45.7	8	14	US-10-140-164-39	Sequence 39, Appl
45	21	45.7	8	14	US-10-006-869-2160	Sequence 2160, App

ALIGNMENTS

RESULT 1
US-09-761-636A-6
; Sequence 6, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6

Query Match 100.0%; Score 46; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CNEESLIC 8
Db 1 CNEESLIC 8

RESULT 2
US-09-761-636A-20
; Sequence 20, Application US/09761636A
; Patent No. US20020065218A1

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; TYPE: PRT
; LENGTH: 8
; ORGANISM: synthetic construct
US-09-761-636A-19

Query Match 89.1%; Score 41; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CNEESLIC 8

RESULT 5
US-09-761-636A-21
; Sequence 21, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; TYPE: PRT
; LENGTH: 8
; ORGANISM: synthetic construct
US-09-761-636A-21

Query Match 84.8%; Score 39; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CNEESLIC 8

RESULT 6
US-09-795-006A-133
; Sequence 133, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; TYPE: PRT
; LENGTH: 8
; ORGANISM: synthetic construct
US-09-761-636A-20

Query Match 93.5%; Score 43; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CNEESLIC 8

RESULT 3
US-09-761-636A-22
; Sequence 22, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; TYPE: PRT
; LENGTH: 8
; ORGANISM: synthetic construct
US-09-761-636A-22

Query Match 91.3%; Score 42; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CNEESVVC 8

RESULT 4
US-09-761-636A-19
; Sequence 19, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela

; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-795-006A-133

Query Match 56.5%; Score 26; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESL 6
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Db 3 CNDEGL 8

RESULT 7
US-10-363-208-108
; Sequence 108, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-108

Query Match 54.3%; Score 25; DB 12; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : | : |
Db 1 CSRSFLC 8

RESULT 8
US-09-795-006A-142
; Sequence 142, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-795-006A-142

Query Match 52.2%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESL 6
| : | : |
Db 3 CNSEGL 8

RESULT 9
US-09-827-345-14
; Sequence 14, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: LE CONTEL, CAROLE
; APPLICANT: GALEA, PASCALE
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: 065691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-14

Query Match 50.0%; Score 23; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEES 5
| : | : |
Db 2 CNPES 6

RESULT 10
US-09-840-277-25
; Sequence 25, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394

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; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-457

Query Match          50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CWDDGLMC 8

RESULT 13
US-10-363-208-74
; Sequence 74, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-74

Query Match          50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CRASAMVC 8

RESULT 14
US-10-363-208-82
; Sequence 82, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-82

Query Match          50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-25

Query Match          50.0%; Score 23; DB 9; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CWDDGLMC 8

RESULT 11
US-09-185-908-115
; Sequence 115, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-115

Query Match          50.0%; Score 23; DB 9; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CRTSSYVC 8

RESULT 12
US-10-609-217-457
; Sequence 457, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
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QY 1 CNEESLIC 8
| : : : |
Db 1 CRASAMVC 8

RESULT 15
US-10-632-388-457
; Sequence 457, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 457
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-457

Query Match 50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 37.5%; Pred No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
| : : : |
Db 1 CWDGGLMC 8

Search completed: September 5, 2004, 10:44:41
Job time : 67 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:37:23 ; Search time 20 Seconds
(without alignments)
20.650 Million cell updates/sec

Title: US-09-761-636A-6
Perfect score: 46
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 71086

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	65.2	8	US-09-100-409A-27	Sequence 27, Appl
2	26	56.5	8	US-09-089-878-3	Sequence 3, Appl
3	25	54.3	8	US-08-397-633A-100	Sequence 100, Appl
4	25	54.3	8	US-09-258-754-49	Sequence 49, Appl
5	25	54.3	8	US-09-042-107-49	Sequence 49, Appl
6	25	54.3	8	US-09-722-250D-49	Sequence 49, Appl
7	23	50.0	7	US-08-973-551-14	Sequence 14, Appl
8	23	50.0	8	US-08-520-535-3	Sequence 3, Appl
9	23	50.0	8	US-09-079-432-3	Sequence 3, Appl
10	23	50.0	8	US-09-258-754-33	Sequence 33, Appl
11	23	50.0	8	US-09-258-754-42	Sequence 42, Appl
12	23	50.0	8	US-09-258-754-214	Sequence 214, Appl
13	23	50.0	8	US-09-042-107-33	Sequence 33, Appl
14	23	50.0	8	US-09-042-107-42	Sequence 42, Appl
15	23	50.0	8	US-09-042-107-214	Sequence 214, Appl
16	23	50.0	8	US-08-160-604-79	Sequence 79, Appl
17	23	50.0	8	US-08-160-604-80	Sequence 80, Appl
18	23	50.0	8	US-09-722-250D-33	Sequence 33, Appl
19	23	50.0	8	US-09-722-250D-42	Sequence 42, Appl
20	23	50.0	8	US-09-722-250D-214	Sequence 214, Appl
21	23	50.0	8	US-09-428-082B-457	Sequence 457, Appl
22	22	47.8	6	US-09-187-859-3664	Sequence 3664, Ap
23	22	47.8	6	US-09-839-542B-3664	Sequence 3664, Ap
24	22	47.8	7	US-09-187-859-3665	Sequence 3665, Ap
25	22	47.8	7	US-09-839-542B-3665	Sequence 3665, Ap
26	22	47.8	8	US-09-258-754-36	Sequence 36, Appl
27	22	47.8	8	US-09-258-754-48	Sequence 48, Appl

28 22 47.8 8 3 US-09-258-754-256 Sequence 256, App
29 22 47.8 8 3 US-09-042-107-36 Sequence 36, Appl
30 22 47.8 8 3 US-09-042-107-48 Sequence 48, Appl
31 22 47.8 8 3 US-09-042-107-256 Sequence 256, App
32 22 47.8 8 4 US-09-187-859-1071 Sequence 1071, Ap
33 22 47.8 8 4 US-09-187-859-3624 Sequence 3624, Ap
34 22 47.8 8 4 US-09-839-542B-1071 Sequence 1071, Ap
35 22 47.8 8 4 US-09-839-542B-3624 Sequence 3624, Ap
36 22 47.8 8 4 US-09-722-250D-36 Sequence 36, Appl
37 22 47.8 8 4 US-09-722-250D-48 Sequence 48, Appl
38 22 47.8 8 4 US-09-722-250D-256 Sequence 256, App
39 22 47.8 8 4 US-09-646-423-11 Sequence 11, Appl
40 21 45.7 5 4 US-09-187-859-3563 Sequence 3663, Ap
41 21 45.7 5 4 US-09-839-542B-3663 Sequence 3663, Ap
42 21 45.7 6 4 US-09-187-859-985 Sequence 985, App
43 21 45.7 6 4 US-09-187-859-2242 Sequence 2242, Ap
44 21 45.7 6 4 US-09-839-542B-985 Sequence 985, App
45 21 45.7 6 4 US-09-839-542B-2242 Sequence 2242, Ap

ALIGNMENTS

RESULT 1
US-09-100-409A-27
; Sequence 27, Application US/09100409A
; Patent No. 6090388
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND
; TITLE OF INVENTION: IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,409A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-409A-27

Query Match 65.2% Score 30; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CNEESLIC 8

Db 1 CNOGSFLC 8

0; taps


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Db          1  CGNETLRC 8

RESULT 6
US-09-722-250D-49
; Sequence 49, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Issues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-49

Query Match          54.3%; Score 25; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy          1  CNEESLIC 8
Db          1  CGNETLRC 8

RESULT 7
US-08-973-551-14
; Sequence 14, Application US/08973551
; Patent No. 6113902
; GENERAL INFORMATION:
; APPLICANT: Chermann, Jean-Claude
; APPLICANT: Le Contel, Carole
; APPLICANT: Galea, Pascale
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING
; TITLE OF INVENTION: AN INTRACELLULAR PHASE COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,551
; FILING DATE: 30-DEC-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01006
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9507914
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.

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; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 65691/130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-973-551-14

Query Match          50.0%; Score 23; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1  CNEES 5
Db          2  CNPES 6

RESULT 8
US-08-520-535-3
; Sequence 3, Application US/08520535
; Patent No. 5817750
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,535
; FILING DATE: 28-AUG-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-520-535-3

Query Match          50.0%; Score 23; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy          1  CNEESLIC 8
Db          1  CWDGLMC 8

RESULT 9

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US-09-079-432-3
; Sequence 3, Application US/09079432
; Patent No. 5955572
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,432
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/520,535
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-079-432-3

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Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : | : |
Db 1 CWDGGLMC 8

RESULT 10
US-09-258-754-33
; Sequence 33, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-258-754-33

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : | : |
Db 1 CRHESSSC 8

RESULT 11
US-09-258-754-42
; Sequence 42, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-42

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : | : |
Db 1 CHEGLTC 8

RESULT 12
US-09-258-754-214
; Sequence 214, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 214
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-214

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : : : |
Db 1 CFXSTLLC 8

RESULT 13

US-09-042-107-33
; Sequence 33, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-33

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : : : |
Db 1 CRHSSSC 8

RESULT 14

US-09-042-107-42
; Sequence 42, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-42

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : : : |
Db 1 CHEGYLTC 8

RESULT 15

US-09-042-107-214
; Sequence 214, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 214
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-214

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| : : : |
Db 1 CFXSTLLC 8

Search completed: September 5, 2004, 10:40:46
Job time : 20 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:44:49 ; Search time 22 Seconds
(without alignments)
48.096 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

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Total number of hits satisfying chosen parameters: 1327

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	36.1	11	2 D57789	gallbladder stone
2	20	32.8	6	2 I65546	MHC H2-L antigen - mouse (fragment)
3	19	31.1	5	2 A60521	glycogen phosphory
4	18	29.5	10	2 C39191	hypothetical prote
5	17	27.9	8	2 G33098	205K exoantigen -
6	17	27.9	10	2 C39111	IG heavy chain C r
7	17	27.9	10	2 PH0944	T-cell receptor be
8	17	27.9	11	2 S21727	gamma-interferon-1
9	17	27.9	11	2 PH0929	T-cell receptor be
10	16	26.2	4	2 I51049	metallothionein-A
11	16	26.2	9	2 A60356	118K stomach cance
12	16	26.2	9	2 PT0247	IG heavy chain CRD
13	16	26.2	10	2 S62880	polygalacturonase
14	16	26.2	10	2 A61622	vitellogenin, 190k
15	16	26.2	10	2 PH0926	T-cell receptor be
16	16	26.2	10	2 A32195	Tachykinin II - mi
17	16	26.2	11	1 ECLQ2M	paraspinal crystal
18	16	26.2	11	2 S00616	peptide-N4-(N-acet
19	15	24.6	10	2 B59272	IG H chain V-D-J r
20	15	24.6	11	2 PH1584	stathmin - mouse (
21	15	24.6	11	2 PH0042	T-cell receptor be
22	15	24.6	11	2 PH0941	major protein anti
23	14	23.0	5	2 E60274	hypothetical colla
24	14	23.0	6	4 A35039	large granule L3 c
25	14	23.0	7	2 PC1316	hypertrehalosemic
26	14	23.0	8	2 S08996	adipokinetic hormo
27	14	23.0	8	2 B49823	neuropeptide Led-C
28	14	23.0	8	2 B44960	adipokinetic hormo
29	14	23.0	8	2 A33995	

30 14 23.0 8 2 PL0184 capsid protein VP-
31 14 23.0 8 2 A42057 fibroblast growth
32 14 23.0 8 2 A35180 neutral proteinase
33 14 23.0 9 2 B41983 orf downstream to b
34 14 23.0 9 2 A29477 diuretic neuropept
35 14 23.0 9 2 I52974 seminal vesicle pr
36 14 23.0 10 1 XAVI6B angiotensin-conver
37 14 23.0 10 2 JCI416 hypertrehalosemic
38 14 23.0 10 2 S09138 hypertrehalosemic
39 14 23.0 10 2 B33995 hypertrehalosemic h
40 14 23.0 10 2 PC2171 triacylglycerol li
41 14 23.0 10 2 PA0050 protein QA100052 -
42 14 23.0 10 2 B61218 alpha-gliadin 6Ha
43 14 23.0 10 2 E86128 hypohetical prote
44 14 23.0 11 1 XASNBA bradykinin-potent
45 14 23.0 11 2 S58244 pyrroloquinoline q

ALIGNMENTS

RESULT 1

D57789
gallbladder stone matrix protein, 14.5K - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996
C:Accession: D57789

R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A:Description: The proteins of gallbladder stones.

A:Reference number: A57789
A:Accession: D57789
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <BIN>

Query Match 36.1%; Score 22; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
| | | | |
DB 1 PATSAP 6

RESULT 2

I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234

Query Match 32.8%; Score 20; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VPC 11
| | | | |
DB 2 VPC 4

RESULT 3

A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

N:Alternate names: glycogen phosphorylase b
 C:Species: Liza ramada
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
 C:Accession: A60521
 R:Bonamusa, L.; Baanante, I.V.
 Comp. Biochem. Physiol. B 95, 295-301, 1990
 A:Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
 A:Reference number: A60521; PMID:90227907; PMID:2109669
 A:Accession: A60521
 A:Molecule type: protein
 A:Residues: 1-5 <BN>
 C:Superfamily: glucan phosphorylase
 C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
 F3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 31.1%; Score 19; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVP 5
 ||||
 Db 2 ISVP 5

RESULT 4

C39191
 Hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis
 C:Species: Bacteroides fragilis
 C:Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
 C:Accession: C39191
 R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.
 J. Bacteriol. 173, 176-183, 1991
 A:Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra
 A:Reference number: A39191; PMID:91100280; PMID:1846135
 A:Accession: C39191
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-10 <SE>
 A:Cross-references: GB:M37699

Query Match 29.5%; Score 18; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 3.8e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
 ||||
 Db 4 SREWTSI 10

RESULT 5

G33098
 20SK exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: G33098
 R:Nichols, J.H.; Hager, L.P.
 Submitted to the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: G33098
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <NIC>

Query Match 27.9%; Score 17; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLTSV 9
 ||||
 Db 2 VPLXLV 7

RESULT 6

C39111

Ig heavy chain C region - Pacific hagfish (fragment)
 C:Species: Eptatretus stouti (Pacific hagfish)
 C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
 C:Accession: C39111
 R:Varner, J.; Neame, P.; Litman, G.W.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
 A:Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil
 A:Reference number: A39111; PMID:91156684; PMID:2000382
 A:Accession: C39111
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <VAR>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 5.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISVPL 6
 ||||
 Db 4 ISSPL 8

RESULT 7

PH0944
 T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C:Accession: PH0944
 R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
 A:Reference number: PH0891; PMID:92078957; PMID:1836012
 A:Accession: PH0944
 A:Molecule type: mRNA
 A:Residues: 1-10 <GOL>
 A:Experimental source: complete Freund's adjuvant-immunized lymph node
 A>Note: the authors translated the codon GAC for residue 9 as Glu
 C:Keywords: T-cell receptor

Query Match 27.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CJSVP 5
 ||||
 Db 1 CASSP 5

RESULT 8

S21727
 gamma-interferon-induced protein IP-30 precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C:Accession: S21727
 R:Wei, M.L.; Cresswell, P.
 Nature 356, 443-446, 1992
 A:Title: HLA-A2 molecules in an antigen-processing mutant cell contain signal sequence
 A:Reference number: S21727; PMID:92212461; PMID:1557127
 A:Accession: S21727
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <WEI>

Query Match 27.9%; Score 17; DB 2; Length 11;
 Best Local Similarity 37.5%; Pred. No. 6.2e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISVPLTSV 9
 :|||:
 Db 3 LDVPTAAV 10

RESULT 9
PH0929
T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0929
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0929
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
C:Keywords: T-cell receptor

Query Match 27.9%; Score 17; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CDSVPLT 7
| | | | |
Db 1 CASRPGT 7

RESULT 10
I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) me
A:Reference number: I51049; MUID:95324545; PMID:7601121
A:Accession: I51049
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:gl019799; PIDN:CA56466.1; PID:g4379328

Query Match 26.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11
| | |
Db 3 PC 4

RESULT 11
A60356
118K stomach cancer antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C:Accession: A60356
R:Shiraishi, Y.
Int. J. Cancer 45, 783-787, 1990
A:Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A:Reference number: A60356; MUID:90216080; PMID:2323853
A:Accession: A60356
A:Molecule type: protein
A:Residues: 1-9 <SHI>
C:Keywords: glycoprotein

Query Match 26.2%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLTSV 9
| | | | |
Db 1 IPLKPV 6

RESULT 12

PT0247
IG heavy chain CRD3 region (clone 2-106A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0247
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0247
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.2%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTS 8
| | | | |
Db 2 SAPIDS 7

RESULT 13

S62880
polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
C:Species: Aspergillus sp.
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S62880
R:Stratillova, E.; Dzurkova, M.; Markovic, O.; Joernvall, H.
FEBS Lett. 382, 164-166, 1996
A:Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A:Reference number: S62880; MUID:96196586; PMID:8612742
A:Accession: S62880
A:Molecule type: protein
A:Residues: 1-10 <STR>
C:Keywords: glycosidase; hydrolase
F:4/Active site: Tyr #status predicted

Query Match 26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11
| | |
Db 9 PC 10

RESULT 14

A61622
vitellogenin, 190k chain - gypsy moth (fragment)
N:Contains: vitellin
C:Species: Lymantria dispar (gypsy moth)
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
C:Accession: A61622
R:Hiremath, S.; Eshita, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
A:Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantri
A:Reference number: A61622
A:Accession: A61622
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <HIR>
C:Keywords: egg yolk; hemolymph

Query Match 26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLT 7
| |
Db 2 PLT 4

RESULT 15
PH0926
T-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0926
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0926
A:Molecule type: mRNA
A:Residues: 1-10 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
A>Note: the authors translated the codon AGA for residue 4 as Thr
C:Keywords: T-cell receptor

Query Match 26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. NO. 8.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CUSVP 5
| |
Db 1 CASRP 5

Search completed: September 5, 2004, 10:48:24
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:40:49 ; Search time 15 seconds
(without alignments)
38.185 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 441

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	23	37.7	11	1	TIN4_HOPTI	P82654 hoplobatrach
2	19	31.1	11	1	TIN1_HOPTI	P82651 hoplobatrach
3	18	29.5	8	1	COM2_CONPU	P59785 conus purpu
4	17.5	28.7	9	1	MGMT_BOVIN	P29177 bos taurus
5	17	27.9	10	1	UPA4_HUMAN	P30090 homo sapien
6	16	26.2	11	1	CXIL_HUMAN	P58807 conus marmo
7	15	24.6	10	1	LPK2_LOCOMI	P41488 locusta mig
8	14	23.0	8	1	AKH_TABAT	P14595 tabanus atr
9	14	23.0	8	1	HTF2_PERAM	P04549 periplaneta
10	14	23.0	8	1	UPA4_HUMAN	P30096 homo sapien
11	14	23.0	9	1	DNF1_LOCOMI	P16339 locusta mig
12	14	23.0	9	1	YBER_AZOVI	P25825 azotobacter
13	14	23.0	10	1	BPP2_BOTUA	P01022 bothrops ja
14	14	23.0	10	1	HTF2_CARMO	P11385 carausius m
15	14	23.0	10	1	HTF_TABAT	P14596 tabanus atr
16	14	23.0	11	1	BPP3_BOTIN	P30423 bothrops in
17	14	23.0	11	1	BPP4_BOTIN	P30424 bothrops in
18	14	23.0	11	1	BPPB_AGHA	P01021 agkistrodon
19	14	23.0	11	1	PQOC_PSEFL	P55173 pseudomonas
20	13	21.3	6	1	E101_LITRU	P82096 litoria rub
21	13	21.3	8	1	UPA1_HUMAN	P30087 homo sapien
22	13	21.3	9	1	CONO_CONST	P05487 conus stria
23	13	21.3	10	1	BPP2_BOTIN	P30422 bothrops in
24	13	21.3	10	1	BPP_VIPAS	P31351 vipera aspi
25	13	21.3	10	1	COXH_ONCMY	P80331 oncorhynch
26	13	21.3	10	1	COXQ_SHEEP	P80337 ovis aries
27	13	21.3	10	1	ESTA_SCHGA	P81012 schizaphis
28	13	21.3	10	1	NS1_MVCTU	P81135 mycobacteri
29	12	19.7	7	1	TPFY_PACDA	P83455 pachymedusa
30	12	19.7	8	1	ALL6_CYPDO	P82157 cydia pomon
31	12	19.7	8	1	FUSS_FUSSO	P81010 fusarium so
32	12	19.7	8	1	VGLG_HSV2B	P81780 herpes simp
33	12	19.7	9	1	FAR5_PENNO	P83320 penaeus mon

34 12 19.7 9 1 FLA2_TREHY P80159 treponema h
35 12 19.7 9 1 OXYT_BUFRE P42995 bufo regula
36 12 19.7 9 1 SAP_STOVA P24047 stomopneute
37 12 19.7 10 1 TKL2_LOCOMI P16224 locusta mig
38 12 19.7 10 1 UPA8_HUMAN P30094 homo sapien
39 12 19.7 11 1 T2P1_PROVU P31031 proteus vul
40 11 18.0 6 1 VP19_HSVIK P23210 herpes simp
41 11 18.0 7 1 CARP_MYTED P10420 mytilus edu
42 11 18.0 7 1 MNP1_LEPDE P42984 leptinotars
43 11 18.0 8 1 PKP3_PERAM P82618 periplaneta
44 11 18.0 9 1 COXE_THUOB P80375 thunnus obe
45 11 18.0 9 1 FAR9_ASCSU P43172 ascaris suu

ALIGNMENTS

RESULT 1
TIN4_HOPTI
ID TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagakaj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina".
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=WALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;
Query Match 37.7%; Score 23; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CISVPL 6
Db 3 CYAIPL 8
RESULT 2
TIN1_HOPTI
ID TIN1_HOPTI STANDARD; PRT; 11 AA.
AC P82651;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tigerin-1.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;

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RX PubMed-11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaran N.;
RT "Tigerlins: novel antimicrobial peptides from the Indian frog Rana
RL tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
FT DISULFID 2 10
FT MOD_RES 11 11
FT SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;
SQ
Query Match 31.1%; Score 19; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 9.7e+02;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CISVPL 6
Db | : | :
2 CTMIPI 7
RESULT 3
COM2_CONPU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9938839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: Belongs to the contryphan family.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD_RES 4 4
FT SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
SQ
Query Match 29.5%; Score 18; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CISVP 5
Db | : | :
2 CVLLP 6
RESULT 4
MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
```

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DE methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Kazran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically
CC transferring the alkyl group at the O-6 position to a cysteine
CC residue in the enzyme. This is a suicide reaction: the enzyme is
CC irreversibly inactivated.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro: IPR001497; Methyltransf_1.
DR PROSITE: PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9
FT NON_TER 9 9
FT SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;
SQ
Query Match 28.7%; Score 17.5; DB 1; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 4 VPLTSVPC 11
Db | : | :
3 IPILT-PC 9
RESULT 5
UPAA_HUMAN STANDARD; PRT; 10 AA.
AC P30090;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.8, its MW is: 40.5 kDa.
CC -!- MISCELLANEOUS: This spot is on a position thought to be that of
CC Zn-alpha-2 glycoprotein, but it does not correspond to that
CC protein.
DR SWISS-2DPAGE; P30090; HUMAN.
FT NON_TER 1 1
FT UNSURE 4 4
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;
SQ
```

Query Match 27.9%; Score 17; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLTS 8
 DB 2 VPNTS 6

RESULT 6
 ID CKL1 CONMR STANDARD; PRT; 11 AA.
 AC P58807;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda-conotoxin CmrVIA.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji K.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the
 RT venom of Conus marmoreus";
 RL J. Biol. Chem. 275:39516-39522 (2000).
 CC -!- FUNCTION: Inhibits the neuronal noradrenergic transporter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1237.93; MW ERR=0.21; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 2 11
 FT DISULFID 3 8
 FT MOD RES 10 10 HYDROXYLATION.
 SQ SEQUENCE 11 AA; 1226 MW; 277AC60B7232B58 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11
 DB 10 PC 11

RESULT 7
 ID LPK2 LOCM1 STANDARD; PRT; 10 AA.
 AC P4148;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94094539; PubMed=7903606;
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustapyrokinin II from
 RT Locusta migratoria, another member of the FXPRL-amide peptide

RT family";
 RL Comp. Biochem. Physiol. 106C:103-109 (1993).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro: IPR001484; PYROKININ.
 DR PROSITE: PS00539; PYROKININ.
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVP 5
 DB 2 SVP 4

RESULT 8
 ID AKH TABAT STANDARD; PRT; 8 AA.
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
 DE (DCC I).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 OC Tabanus.
 OX NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera)";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR PIR; A33995; A33995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LTSVP 10
 DB 2 LTSVP 6

RESULT 9
 ID HTF2 PERAM STANDARD; PRT; 8 AA.
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)

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RESULT 10
UPAA HUMAN
ID UPAA HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DC 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1] RN SEQUENCE.
RP TISSUE=Plasma;
RC MEDLINE=93092937; PubMed=1459097;
RX Hughes G.J., Frutiger S., Faquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 7, its MW is: 12 kDa.
CC SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1
FT VARIANT 5
FT FT 5 F -> P.
FT NON_TER 8 8 /FTIG=VAR_000004.
FT SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;
SQ
Query Match 23.0%; Score 14; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLTSVP 10
DB 1 VILTFYP 7

RESULT 11
DNFI_LOCFI
ID DNFI_LOCFI STANDARD; PRT; 9 AA.
AC P16339;
DC 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locupressin (Diuretic neuropeptide F1/F2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OC NCBI_TaxID=7004;
[1] RN SEQUENCE.
RP TISSUE=Suboesophageal ganglion, and Thoracic ganglion;
RC MEDLINE=98077077; PubMed=3689410;
RX Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA Delaage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone F1
Locusta migratoria.";
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -!- FUNCTION: DIURETIC HORMONE.
CC -!- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; A29477; A29477.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4.1.
DR PROSITE; PS02264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation.
FT DISULFID 1 6 IN FL.
FT DISULFID 1 1 INTERCHAIN (WITH C-6) (IN F2).
FT DISULFID 6 6 INTERCHAIN (WITH C-1) (IN F2).
FT MOD_RES 9 9 AMIDATION.

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SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match      23.0%; Score 14; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 LRSVP 10
   :|:|
Db 3 ITNCP 7

RESULT 12
YBFR_AZOVI
ID YBFR_AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3'region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RT Stiefel E.I.;
RL "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M83692; AAA22122.1;
DR PIR; B41983;
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 9 AA; 947 MW; DF98BSA1B41776D CRC64;

Query Match      23.0%; Score 14; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTS 8
   |||
Db 4 PRTPS 7

RESULT 13
BPP2_BOTJA
ID BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE inhibitor V-6-11).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RC MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,

SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match      23.0%; Score 14; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 7.1e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PLTSVP 10
   | | |
Db 4 PRQIP 9

RESULT 14
HTF2_CARMO
ID HTF2_CARMO STANDARD; PRT; 10 AA.
AC P11385;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor II (HTF-II) (HPTH-II) (Hypertrehalosaemic
DE neuropeptide II).
OS Carausius morosus (Indian stick insect), and
OS Extatosoma tiaratum (Stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatodea;
OC Heteronemidae; Carausius.
OX NCBI_TaxID=7022, 7024;
RN [1]
RP SEQUENCE.
RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=87157103; PubMed=3828078;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structure of the hypertrehalosaemic factor II from the
RT corpus cardiaca of the Indian stick insect, Carausius morosus,
RT determined by fast atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP CARBOHYDRATE-LINKAGE SITE.
RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=93129188; PubMed=1482345;
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT a stick insect corpus cardiaca.";
RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- major carbohydrate in the hemolymph of insects).
CC -1- MASS SPECTROMETRY: MW=1308.61; METHOD=PAB.
CC -1- SIMILARITY: Belongs to the AKH / HPTH / RPCH family.
DR PIR; JCI416; JCI416.
DR PIR; S09138; S09138.
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DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LTSVP 10
DB 2 LTFTP 6

RESULT 15
HTF_TABAT STANDARD; PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II) (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosaemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HPTH / RPCH family.
DR PIR; B33995; B33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LTSVP 10
DB 2 LTFTP 6

Search completed: September 5, 2004, 10:46:52
Job time : 15 secs
```

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:43:34 ; Search time 58 Seconds
(without alignments)
59.840 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1903

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	34.4	11	6 Q9TQSO	Q9tqs0 bos taurus
2	20	32.8	8	2 Q8GMMS	Q8gmms acinetobact
3	20	32.8	10	15 Q85598	Q85598 moloney mur
4	20	32.8	10	15 Q85563	Q85563 moloney mur
5	20	32.8	10	15 Q85619	Q85619 moloney mur
6	19	31.1	8	2 Q56140	Q56140 streptococ
7	19	31.1	10	8 Q9TKF7	Q9tkf7 agonis gran
8	19	31.1	10	8 Q9TKF9	Q9tkf9 melaleuca v
9	19	31.1	10	8 Q9TKG2	Q9tkg2 callistemon
10	19	31.1	10	8 Q9TKF1	Q9tkf1 homalosperm
11	19	31.1	10	8 Q9TKF8	Q9tkf8 tristanlops
12	19	31.1	10	8 Q9TKF4	Q9tkf4 angasomyrtu
13	19	31.1	10	8 Q9TKF3	Q9tkf3 asteromyrtu
14	19	31.1	10	8 Q9TKF0	Q9tkf0 neofabricia
15	19	31.1	10	8 Q9TKF0	Q9tkf0 kunzea ambi
16	19	31.1	10	8 Q9TKF6	Q9tkf6 agonis obtu

17	19	31.1	10	8 Q9THM7	Q9thm7 leptospermu
18	19	31.1	10	8 Q9TKB2	Q9tkb2 leptospermu
19	19	31.1	10	8 Q9TKB3	Q9tkb3 leptospermu
20	19	31.1	10	8 Q9TKB7	Q9tkb7 kunzea pulc
21	19	31.1	10	8 Q9THM6	Q9thm6 leptospermu
22	19	31.1	10	8 Q9TKB6	Q9tkb6 leptospermu
23	19	31.1	10	8 Q9TKB8	Q9tkb8 kunzea eric
24	19	31.1	10	8 Q9TKB9	Q9tkb9 kunzea baxt
25	19	31.1	10	8 Q9TKB1	Q9tkb1 neofabricia
26	19	31.1	10	8 Q9TKB4	Q9tkb4 leptospermu
27	19	31.1	10	8 Q9TKG0	Q9tkg0 lophostemon
28	19	31.1	11	10 P83092	P83092 spinacia ol
29	18	29.5	9	10 Q9FXL0	Q9fxl0 lilium long
30	18	29.5	11	4 Q9NYF38	Q9nyf38 homo sapien
31	18	29.5	11	11 Q99N81	Q99n81 mus musculu
32	17	27.9	8	2 Q8KFX4	Q8kfx4 microcystis
33	17	27.9	9	2 Q9K4M6	Q9k4m6 staphylococ
34	17	27.9	9	10 Q7X6A3	Q7x6a3 zea mays su
35	17	27.9	10	8 Q96041	Q96041 oenothera b
36	17	27.9	10	10 Q7Y0I8	Q7y0i8 zea mays su
37	17	27.9	10	12 Q39957	Q39957 hepatitis g
38	17	27.9	11	7 Q77872	Q77872 oreochromis
39	17	27.9	11	7 Q77873	Q77873 oreochromis
40	17	27.9	11	7 Q77871	Q77871 oreochromis
41	17	27.9	11	11 Q91Y49	Q91y49 mus musculu
42	16	26.2	8	2 Q849P4	Q849p4 salmonella
43	16	26.2	8	4 Q16468	Q16468 homo sapien
44	16	26.2	8	6 Q02831	Q02831 oryctolagus
45	16	26.2	8	6 Q9TRY3	Q9try3 sus sp. ins

ALIGNMENTS

RESULT 1
Q9TQSO PRELIMINARY; PRT; 11 AA.
AC Q9TQSO; 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-MAY-2000 (TREMREL. 13, Last annotation update)
DE C-KIT (Fragment).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
RT "A polymorphism in the bovine c-kit gene."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243424; CAB60775.1; -
DR EMBL; AJ243060; CAB60774.1; -
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 34.4%; Score 21; DB 6; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SVPLTSV 9
Db 3 AVPVSV 9

RESULT 2
Q8GMMS PRELIMINARY; PRT; 8 AA.
ID Q8GMMS
AC Q8GMMS;
DT 01-MAR-2003 (TREMREL. 23, Created)

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DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Transposase (Fragment).
GN TNPl7.
OS Acinetobacter sp. BW3.
OG Plasmid pKlH207.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=106395;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3; PLASMID=pKlH207;
RA Kholodii G.Y., Yuriyeva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKlH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3; PLASMID=pKlH207;
RA Kholodii G.Y., Mindlin S.Z., Gorlenko Z.M., Yuriyeva O.V.,
RA Petrova M.A., Nikiforov V.G.;
RT "A young family of transposable adaptive DNA segments identified in
RT the Acinetobacter genus.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250234; CAC80784.1; -.
DR EMBL; AJ486856; CAD31078.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 8 AA; 911 MW; 2D71B2D6C1A7377A CRC64;

Query Match 32.8%; Score 20; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSV 9
Db 2 PLTQV 6

RESULT 3
Q85598 PRELIMINARY; PRT; 10 AA.
AC Q85598;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain HT1) env/mos 5' junction
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03106; AAA46492.1; -.
DR NON_TER 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 32.8%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SVPC 11
Db 4 STPC 7

RESULT 4
Q85563 PRELIMINARY; PRT; 10 AA.
AC Q85563;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env-mos fusion protein (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=82196891; PubMed=6281735;
RA Donoghue D.J., Hunter T.;
RT "A generalized method of subcloning DNA fragments by restriction site
RT reconstruction: Application to sequencing the amino-terminal region of
RT the transforming gene of Gazdar murine sarcoma virus.";
RL Nucleic Acids Res. 10:2549-2564(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03105; AAA46491.1; -.
DR NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1062 MW; F9ECFCBEA771B5B1 CRC64;

Query Match 32.8%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
Db 4 STPC 7

RESULT 5
Q85619 PRELIMINARY; PRT; 10 AA.
AC Q85619;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain ml) env/mos 5' junction
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03108; AAA46494.1; -.
DR NON_TER 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 32.8%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SVPC 11
Db 4 STPC 7

RESULT 6
Q56140

```


ID Q56140 PRELIMINARY; PRT; 8 AA.
 AC Q56140;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE STP6 protein (Fragment).
 GN STP6.
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1308;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Str11;
 RX MEDLINE=95047254; PubMed=7958782;
 RA Constable A., Mollet B.;
 RT "Isolation and characterisation of promoter regions from Streptococcus
 thermophilus". Lett. 122:85-90(1994).
 RL FEMS Microbiol. Lett. 122:85-90(1994).
 DR EMBL; X78210; CAA55045.1; -;
 FT NON TER 8
 SQ SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;
 Query Match 31.1%; Score 19; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ISVP 5
 Db |||||
 3 ISVP 6
 RESULT 7
 Q9TKF7 PRELIMINARY; PRT; 10 AA.
 ID Q9TKF7;
 AC Q9TKF7;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE AtPB (Fragment).
 GN AtPB.
 OS Agonis grandiflora.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Agonis.
 OX NCBI_TaxID=106028;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL; AF184675; AAF03845.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
 Query Match 31.1%; Score 19; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 PLTSVP 10
 Db |||||
 5 PTTSRP 10
 RESULT 8
 Q9TKF9 PRELIMINARY; PRT; 10 AA.
 ID Q9TKF9;
 AC Q9TKF9;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DE AtPB (Fragment).
 GN AtPB.

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE AtPB (Fragment).
 GN AtPB.
 OS Melaleuca viridiflora.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Melaleuca.
 OX NCBI_TaxID=106062;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL; AF184670; AAF03840.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1144 MW; 028C2CA1B1B76440 CRC64;
 Query Match 31.1%; Score 19; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 PLTSVP 10
 Db |||||
 5 PTTSRP 10
 RESULT 9
 Q9TKG2 PRELIMINARY; PRT; 10 AA.
 ID Q9TKG2;
 AC Q9TKG2;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE AtPB (Fragment).
 GN AtPB.
 OS Callistemon polandii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Callistemon.
 OX NCBI_TaxID=73732;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL; AF184666; AAF03836.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
 Query Match 31.1%; Score 19; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 PLTSVP 10
 Db |||||
 5 PTTSRP 10
 RESULT 10
 Q9TKF1 PRELIMINARY; PRT; 10 AA.
 ID Q9TKF1;
 AC Q9TKF1;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE AtPB (Fragment).
 GN AtPB.

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OS Homalospermum firmum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Homalospermum.
OX NCBI_TaxID=106039;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184682; AAF03852.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 PTTSRP 10

RESULT 11
Q9TKF8 PRELIMINARY; PRT; 10 AA.
AC Q9TKF8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN AtPB.
OS Tristaniopsis laurina.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Tristaniopsis.
OX NCBI_TaxID=106073;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184672; AAF03842.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1126 MW; 15132CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 PTTSRP 10

RESULT 12
Q9TKF4 PRELIMINARY; PRT; 10 AA.
AC Q9TKF4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN AtPB.
OS Angasomyrtus salina.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Angasomyrtus.
OX NCBI_TaxID=106032;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184678; AAF03848.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

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Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 5 PLTSVP 10
DB 5 PTTSRP 10

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RESULT 13
Q9TKF3 PRELIMINARY; PRT; 10 AA.
AC Q9TKF3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN AtPB.
OS Asteromyrtus brassii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Asteromyrtus.
OX NCBI_TaxID=106034;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:621-628(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Heslewood M., Quinn C.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184679; AAF03849.2; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

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```

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 5 PLTSVP 10
DB 5 PTTSRP 10

```

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RESULT 14
Q9TKE0 PRELIMINARY; PRT; 10 AA.
ID Q9TKE0;
AC Q9TKE0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE AtPB (Fragment).
GN ATPB.
OS Neofabricia sericisepala.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Neofabricia.
OX NCB1_TaxID=106065;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184700; AAF03869.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match      31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 FTTSRP 10

RESULT 15
O9TKF0 PRELIMINARY; PRT; 10 AA.
AC Q9TKF0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN ATPB.
OS Kunzea ambigua (Tick bush).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Kunzea.
OX NCB1_TaxID=106041;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184683; AAF03853.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match      31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 FTTSRP 10

Search completed: September 5, 2004, 10:47:58
Job time : 60 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:40:24 ; Search time 64 Seconds
(without alignments)
48.563 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 C1SVPLTGVPC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 348779

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	AAU04526	Aau04526 VEGF base
2	59	96.7	11	AAU04542	Aau04542 VEGF base
3	57	93.4	11	AAU04545	Aau04545 VEGF base
4	54	88.5	11	AAU04543	Aau04543 VEGF base
5	52	85.2	11	AAU04544	Aau04544 VEGF base
6	45.5	74.6	10	AAU04532	Aau04532 VEGF base
7	41	67.2	9	AAU04533	Aau04533 VEGF base
8	32	52.5	9	AAU04529	Aau04529 VEGF base
9	30	49.2	8	AAU04518	Aar58418 Partial p
10	30	49.2	9	AAE34703	Aac34703 CAL25/MUC
11	30	49.2	10	AAW12561	Aaw12561 SH2 bindi
12	30	49.2	11	AAW12615	Aaw12615 SH2 bindi
13	29	47.5	11	ABP47579	Abp47579 N. mening
14	29	47.5	11	ABP47580	Abp47580 N. mening
15	27	44.3	10	AAU04532	Aau04532 VEGF base
16	27	44.3	11	ABP47596	Abp47596 N. mening
17	26	42.6	6	AAU04532	Aau04532 VEGF base
18	26	42.6	8	AAU04532	Aau04532 VEGF base
19	26	42.6	9	AAU04532	Aau04532 VEGF base
20	26	42.6	9	AAU04532	Aau04532 VEGF base
21	26	42.6	10	AAU04532	Aau04532 VEGF base
22	26	42.6	10	AAU04532	Aau04532 VEGF base
23	25.5	41.8	9	AAU04532	Aau04532 VEGF base
24	25.5	41.8	9	AAU04532	Aau04532 VEGF base
25	25.5	41.8	9	AAU04532	Aau04532 VEGF base

26	25	41.0	9	2	AAU04526	Aay26264 Isolated
27	25	41.0	9	4	AAE01112	Aae01112 Human leu
28	25	41.0	9	6	ABR24203	AbR24203 Human can
29	25	41.0	9	6	AAE29971	Aae29971 Human air
30	25	41.0	10	2	AAU01720	Aaw01720 Inhibitor
31	25	41.0	10	2	AAU0487	Aar0487 Antibody
32	25	41.0	10	2	AAU88078	Aaw88078 Inhibitor
33	25	41.0	10	2	AAU55214	Aay55214 Anti CD34
34	25	41.0	10	3	AAU86960	Aay86960 Human hae
35	25	41.0	10	3	AAU77429	Aay77429 Fibronect
36	25	41.0	10	4	AAU95853	Aag95853 Human com
37	25	41.0	10	6	ABR24101	AbR24101 Human can
38	25	41.0	10	6	ABR24325	AbR24325 Human can
39	25	41.0	10	6	ABR24347	AbR24347 Human can
40	25	41.0	11	4	AAU00642	Aau00642 Human mem
41	25	41.0	11	7	ADB88785	Adb88785 Membrane
42	24	39.3	6	2	AAU03869	Aar03869 Hypotensi
43	24	39.3	6	4	AAU05003	Aae05003 Human rel
44	24	39.3	6	4	AAU06020	Aab06020 Human MMW
45	24	39.3	7	4	AAU04530	Aau04530 VEGF base

ALIGNMENTS

RESULT 1
AAU04526
ID AAU04526 standard; peptide; 11 AA.
XX AC AAU04526;
XX XX
DT 26-SEP-2001 (first entry)
XX XX
DE VEGF based monocyclic peptide 3.
XX XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1..11 /note= "This bond cyclises the peptide"
XX XX
XX PN WO200152875-A1.
XX XX
XX PD 26-JUL-2001.
XX XX
XX PF 18-JAN-2001; 2001WO-US001533.
XX XX
XX PR 18-JAN-2000; 2000US-0176293P.
XX PR 16-MAY-2000; 2000US-0204590P.
XX XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX XX
XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX XX
XX DR WPI; 2001-442248/47.
XX XX
XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX PT from an exposed loop of a growth factor protein by oxidizing the cysteine
XX PT residues.
XX XX
XX PS Claim 49; Page 32; 102pp; English.
XX XX
XX CC The sequence represents a monomeric monocyclic peptide of the invention,
XX CC whose 3-dimensional structure is modelled on the exposed loop of human
XX CC VEGF (vascular endothelial growth factor). The invention relates to a
XX CC method of producing a monomeric monocyclic peptide by a measuring beta-
XX CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTSVPLTSPVC 11
 |||||
 Db 1 CTSVPLTSPVC 11

RESULT 2
 AAU04542
 ID AAU04542 standard; peptide; 11 AA.
 XX
 AC AAU04542;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 20.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1. .11
 FT /note= "This bond cyclises the peptide"
 XX
 XX WO200152875-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 PI
 XX WPI; 2001-442248/47.
 DR
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT

PT residues.

XX Example 25; Page 47; 102pp; English.

XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 96.7%; Score 59; DB 4; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0034;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTSVPLTSPVC 11
 |||||
 Db 1 CTSVPLTSPVC 11

RESULT 3
 AAU04545
 ID AAU04545 standard; peptide; 11 AA.
 XX
 AC AAU04545;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 23.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1. .11
 FT /note= "This bond cyclises the peptide"
 XX
 XX WO200152875-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX

(LUDW-) LUDWIG INST CANCER RES.
 Achen MG, Hughes RA, Stacker S, Cendron A;
 WPI; 2001-442248/47.
 Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
 Example 25; Page 47; 102pp; English.
 The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the exposed loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty stenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

Query Match 93.4%; Score 57; DB 4; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.0072;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CISVPLTSVPC 11
 |:|||||:
 Db 1 CVSVPLTTVPC 11
 |:|||||:
 RESULT 4
 AAU04543
 ID AAU04543 standard; peptide; 11 AA.
 AC AAU04543;
 DT 26-SEP-2001 (first entry)
 DE VEGF based monocyclic peptide 21.
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..11
 FT /note= "This bond cyclises the peptide"
 XX

PN WO200152875-A1.
 XX 26-JUL-2001.
 PD
 XX 18-JAN-2001; 2001WO-US001533.
 PF
 XX 18-JAN-2000; 2000US-0176293p.
 PR 16-MAY-2000; 2000US-0204590p.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 PI WPI; 2001-442248/47.
 DR
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
 PT
 XX Example 25; Page 47; 102pp; English.
 PS
 XX The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the exposed loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty stenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

Query Match 88.5%; Score 54; DB 4; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.023;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CISVPLTSVPC 11
 |:|||||:
 Db 1 CITIPLTSLPC 11
 |:|||||:
 RESULT 5
 AAU04544
 ID AAU04544 standard; peptide; 11 AA.
 XX
 AC AAU04544;
 XX
 DT 26-SEP-2001 (first entry)
 XX VEGF based monocyclic peptide 22.
 DE Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW
 KW

KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 XX Disulfide-bond 1..11 /note= "This bond cyclises the peptide"
 FT
 FT
 XX WO200152875-A1.
 XX 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Achen MG, Hughes RA, Stackler S, Cendron A;
 PI WPI; 2001-442248/47.
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX

XX Sequence 11 AA;

Query Match 85.2%; Score 52; DB 4; Length 11;
 Best Local Similarity 72.7%; Pred. No; 0.049;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLTSVFC 11
 |||:|||||
 Db 1 C1SLPISVFC 11

RESULT 6
 AAU04532
 ID AAU04532 standard; peptide; 10 AA.

XX AAU04532;
 AC
 XX 26-SEP-2001 (first entry)
 DT
 XX VEGF based monocyclic peptide 10.
 DE
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX Key Location/Qualifiers
 XX Disulfide-bond 1..10 /note= "This bond cyclises the peptide"
 FT
 FT
 XX WO200152875-A1.
 XX 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Achen MG, Hughes RA, Stackler S, Cendron A;
 PI WPI; 2001-442248/47.
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Claim 49; Page 32; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX

XX Sequence 10 AA;

Query Match 74.6%; Score 45.5; DB 4; Length 10;
 Best Local Similarity 90.9%; Pred. No. 0.52;
 Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPLTSVPC 11
 DB 1 CISVPL-SVPC 10

RESULT 7
 AAU04533
 ID AAU04533 standard; peptide; 9 AA.
 XX
 AC AAU04533;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 11.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 PF
 XX 18-JAN-2000; 2000US-0176293P.
 PR
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Achen MG, Hughes RA, Stackner S, Cendron A;
 PI WPI; 2001-442248/47.
 DR
 XX
 PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 PS Claim 49; Page 32; 102pp; English.
 XX

The sequence represents a monomeric monocyclic peptide of the invention,
 whose 3-dimensional structure is modelled on the expose loop of human
 VEGFD (vascular endothelial growth factor). The invention relates to a
 method of producing a monomeric monocyclic peptide by a measuring beta-
 beta carbon separation distances on opposite antiparallel strands of a
 peptide loop fragment from an exposed loop of a growth factor protein and
 cyclising the peptide by oxidising the cysteine residues. The monocyclic
 peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 peptides) and a cyclic peptide with at least one amino acid deleted prior
 to cyclisation are used to interfere with angiogenesis,
 neovascularisation or lymphangiogenesis in a mammal with a condition
 characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 The condition is diabetic retinopathy, psoriasis, arthropathy,
 hemangioma, vascularised malignant or benign tumour, post-recovery
 cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 trauma, substance-induced neovascularisation of the liver, excessive
 hormone-related angiogenic dysfunction, diabetes induced neovascular
 sequelae, hypertension induced neovascular sequelae, or chronic liver
 infection. The peptides are also used to modulate vascular permeability
 in a mammal (the mammal has a condition characterised by fluid
 accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 or brain). The peptides are used to image blood vessels and lymphatic
 vasculature. The monomeric and bicyclic peptides are used to interfere
 with at least one biological activity induced by VEGF, VEGF-C or -D and

CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX

SQ Sequence 9 AA;

Query Match 67.2%; Score 41; DB 4; Length 9;
 Best Local Similarity 81.8%; Pred No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 CISVPLTSVPC 11
 DB 1 CISVPL--VPC 9

RESULT 8
 AAU04529
 ID AAU04529 standard; peptide; 9 AA.
 XX

AC AAU04529;

DT 26-SEP-2001 (first entry)

DE VEGF based monocyclic peptide 7.

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

FH Key Location/Qualifiers

FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"

XX WO200152875-A1.

PD 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stackner S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

PS Claim 49; Page 32; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold

CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ

Sequence 9 AA;

Query Match 52.5%; Score 32; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
 Db 2 SVPLTSV 8
 |||||

RESULT 9
 AAR58418
 ID AAR58418 standard; protein; 8 AA.

XX AAR58418;

AC
 XX
 DT 25-MAR-2003 (revised)
 DT 13-APR-1995 (first entry)

XX Partial peptide 7 from TSAR C46.9-2 binding domain.

XX TSAR; totally synthetic affinity reagent; synthetic; binding domain;
 KW effector domain; concatenated heterofunctional protein; linker; direct;
 KW rapid; detection; screening; treatment; monoclonal antibody; MAb; C46;
 KW anti-carcinoembryonic antigen; anti-CEA.

OS Synthetic.

XX WO9418318-A1.

XX 18-AUG-1994.

XX 01-FEB-1994; 94WO-US000977.

XX 01-FEB-1993; 93US-00013416.

PR 30-DEC-1993; 93US-00176500.

PR 31-JAN-1994; 94US-00189331.

XX (UYN-) UNIV NORTH CAROLINA.

XX Kay EK, Fowlkes DW;

XX WPI; 1994-279739/34.

XX Identifying proteins or peptide(s) which bind a ligand - by screening a
 PT recombinant vector library expressing fusion proteins comprising a
 PT binding domain and an effector domain.

XX Example 7.5; Page 108; 255pp; English.

XX AAR58412-42 are overlapping 8-mer peptides of the binding domain of TSAR
 CC (Totally Synthetic Affinity Reagents) peptide TSAR C46.9-2 (AAR58411).
 CC These bind (partially) a monoclonal antibody, ie. anti-CEA C46 (anti
 CC carcinoembryonic antigen). TSAR peptides are generated using generic
 CC oligonucleotides (see AAQ070470-73 for examples). TSARs are concatenated
 CC heterofunctional proteins or peptides, comprising at least two functional
 CC regions - a binding domain with affinity for a ligand and a second
 CC effector peptide portion that is chemically or biologically active. They
 CC may further comprise a linker peptide between the 2 domains. The TSARs or

CC compens. comprising a TSAR binding domain can be used in vivo to deliver
 CC a chemically or biologically active moiety, eg. metal ion, radioisotope,
 CC peptide, toxin or enzyme, to the specific target or on the cell. They can
 CC also replace the function of macromolecules eg. monoclonal or polyclonal
 CC antibodies and therefore circumvent the need for complex methods of
 CC hybridoma formation or in vivo antibody production. The TSARs are easily
 CC characterised and have designed activity allowing direct and rapid
 CC detection in a screening process. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX

SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVPLTS 8
 Db 1 CVSAPQTS 8
 |||||

RESULT 10
 AAE34703
 ID AAE34703 standard; peptide; 9 AA.

XX AAE34703;

XX 14-MAY-2003 (first entry)

XX CA125/MUC16 O-glycosylation site #1.

XX CA125; antigen; cancer; gene therapy; vaccine; MUC16.

XX Unidentified.

XX WO200292836-A2.

XX 21-NOV-2002.

XX 09-MAY-2002; 2002WO-US014768.

XX 11-MAY-2001; 2001US-0290480P.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Lloyd KO, Yin BWT;

XX WPI; 2003-129305/12.

XX New isolated nucleic acid molecule comprising sequences encoding the
 PT CA125 protein, useful for diagnosing, preventing and/or treating cancer,
 PT e.g. ovarian, pancreatic, breast, endometrial or lung carcinomas.

XX Disclosure; Page 19; 70pp; English.

XX The invention relates to a nucleic acid molecule encoding an ovarian
 CC cancer antigen, CA125. Nucleic acid molecules, vaccine and methods are
 CC useful for diagnosing, preventing and treating cancer, e.g. pancreatic,
 CC lung, ovarian, breast or endometrial carcinoma. The invention is useful
 CC in gene therapy and as vaccines. The present sequence is CA125/MUC16 O-
 CC glycosylation site
 XX

SQ Sequence 9 AA;

Query Match 49.2%; Score 30; DB 6; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTSVP 10
 Db 2 SVPTTSTP 9
 |||||

RESULT 11

AAW12561
ID AAW12561 standard; peptide; 10 AA.
XX
AC AAW12561;
XX
DT 08-APR-1997 (first entry)
XX
DE SH2 binding peptide core sequence #11.
XX
Core peptide; src homology region 2 binding peptide; SH2; cell growth; differentiation; regulation; receptor tyrosine kinase pathway; cancer; signal transduction pathway; non-insulin dependent diabetes;
KW
KW insulin-resistant diabetes.
XX
OS Synthetic.
XX
PN WO9623813-A1.
XX
PD 08-AUG-1996.
XX
PF 31-JAN-1996; 96WO-US001544.
XX
PR 01-FEB-1995; 95US-00382100.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI Patel DV, Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH;
PI Szardenings AK;
XX
DR WPI; 1996-371373/37.
XX
Peptide(s) which bind to SH2 domains - are used to treat diseases associated with aberrant cell growth, differentiation or regulation associated with defects in receptor tyrosine kinase pathways.
XX
Claim 8; Page 116; 203pp; English.
XX
The sequences given in AAW12551-70 represent core peptides of an src homology region 2 (SH2) binding peptide which correspond to the formula: Z7-X-Z8-X X = any D- or L- amino acid; Z7 = phosphotyrosine or its isostere; Z8 = asparagine or its isostere; and the peptide is less than 14 residues in length, with the proviso that if Z7 is phosphotyrosine and Z8 is acylated, then the peptide is not GGGZ7XZ8XPLLL. SH2 binding peptides are used to treat of diagnose cell growth, differentiation or regulation which is associated with defects in receptor tyrosine kinase pathways, by partially blocking or inhibiting a cellular signal transduction pathway. The disease may be cancer, a developmental or differentiation disease or insulin-resistant (or non-insulin dependent) diabetes
XX
SQ Sequence 10 AA;

Query Match 49.2%; Score 30; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. NO. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 C1SVPLT 7
Db 2 C1NVPFT 8

RESULT 12

AAW12615
ID AAW12615 standard; peptide; 11 AA.
XX

AAW12615;
XX
DT 08-APR-1997 (first entry)
XX
DE SH2 binding peptide core sequence #21.
XX
Core peptide; src homology region 2 binding peptide; SH2; cell growth; differentiation; regulation; receptor tyrosine kinase pathway; cancer; signal transduction pathway; non-insulin dependent diabetes;
KW
KW insulin-resistant diabetes.
XX
OS Synthetic.
XX
PN WO9623813-A1.
XX
PD 08-AUG-1996.
XX
PF 31-JAN-1996; 96WO-US001544.
XX
PR 01-FEB-1995; 95US-00382100.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI Patel DV, Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH;
PI Szardenings AK;
XX
DR WPI; 1996-371373/37.
XX
Peptide(s) which bind to SH2 domains - are used to treat diseases associated with aberrant cell growth, differentiation or regulation associated with defects in receptor tyrosine kinase pathways.
XX
Claim 13; Page 117; 203pp; English.

This sequence represents a core peptide of an src homology region 2 (SH2) binding peptide corresponding to the formula: Z7-X-Z8-X X = any D- or L- amino acid; Z7 = phosphotyrosine or its isostere; Z8 = asparagine or its isostere; the amino terminus is acylated, and the peptide is less than 14 residues in length, with the proviso that if Z7 is phosphotyrosine and Z8 is asparagine, then the peptide is not GGGZ7XZ8XPLLL. SH2 binding peptides containing this core peptide are used to treat of diagnose diseases associated with aberrant cell growth, differentiation or regulation which is associated with defects in receptor tyrosine kinase pathways, by partially blocking or inhibiting a cellular signal transduction pathway. The disease may be cancer, a developmental or differentiation disease or insulin-resistant (or non-insulin dependent) diabetes
XX
SQ Sequence 11 AA;

Query Match 49.2%; Score 30; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. NO. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 C1SVPLT 7
Db 2 C1NVPFT 8

RESULT 13

ABP47579
ID ABP47579 standard; peptide; 11 AA.
XX
AC ABP47579;
XX
DT 19-AUG-2002 (first entry)
XX
DE N. meningitidis LOS peptidic mimotope related peptide SEQ ID NO:155.
XX
KW Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS;
KW lipooligosaccharide; monoclonal antibody; antibacterial; infection;
KW antiinflammatory; meningococcal disease.
XX

```

OS Neisseria meningitidis.
XX Synthetic.
XX
XX WO200228888-A2.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-EP011409.
XX
XX 03-OCT-2000; 2000GB-00024200.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX De Bolle XT, Letesson J, Lobet Y, Mertens PY, Poolman J, Voet P;
XX WPI; 2002-479596/51.
XX
XX Novel mimotope of Neisseria meningitidis surface, for treating
XX meningococcal disease, comprising a peptide epitope obtainable by
XX screening peptide library with a specific monoclonal antibody.
XX
XX Claim 15; Page 43; 55pp; English.
XX
XX The present invention describes mimotopes (I) of a surface L3, 7, 9, of
XX meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis
XX comprising a peptide epitope obtained by screening a peptide library with
XX a monoclonal antibody (MAB) like 4BE12C10, H44/24, H44/58, H44/70 or
XX H44/78. (I) is antigenically cross-reactive with MAB. (I) have
XX antibacterial and antiinflammatory activities, and can be used in
XX vaccines. MAB is useful in the identification of (I). (I) or MAB are
XX useful as a medicament, and also in the manufacture of a medicament for
XX treating or preventing meningococcal disease. (I) and MAB are useful for
XX treating a patient suffering from or susceptible to meningococcal disease
XX by administering (I) or MAB to the patient. (I) is useful in a diagnostic
XX assay for meningococcal infection to detect antibodies against L3, 7, 9,
XX LOS and to detect the presence of L3, 7, 9 immunotype meningococcus in a
XX sample from a patient. ABN88464 to ABN88487 and ABP47336 to ABP47754
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 11 AA;
XX
XX Query Match 47.5%; Score 29; DB 5; Length 11;
XX Best Local Similarity 27.3%; Pred. No. 3.1e+02;
XX Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 CTSVPLTSVPC 11
XX |::|
XX 1 CWTIPYRGTC 11
XX
XX Db
XX
XX RESULT 14
XX ABP47580
XX ID ABP47580 standard; peptide; 11 AA.
XX
XX AC ABP47580;
XX
XX 19-AUG-2002 (first entry)
XX
XX N. meningitidis LOS peptidic mimotope related peptide SEQ ID NO:156.
XX
XX Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS;
XX lipooligosaccharide; monoclonal antibody; antibacterial; infection;
XX antiinflammatory; meningococcal disease.
XX
XX Neisseria meningitidis.
XX Synthetic.
XX WO200228888-A2.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-EP011409.
XX
XX 03-OCT-2001; 2001WO-EP011409.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX De Bolle XT, Letesson J, Lobet Y, Mertens PY, Poolman J, Voet P;
XX WPI; 2002-479596/51.
XX
XX Novel mimotope of Neisseria meningitidis surface, for treating
XX meningococcal disease, comprising a peptide epitope obtainable by
XX screening peptide library with a specific monoclonal antibody.
XX
XX Claim 15; Page 43; 55pp; English.
XX
XX The present invention describes mimotopes (I) of a surface L3, 7, 9, of
XX meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis
XX comprising a peptide epitope obtained by screening a peptide library with
XX a monoclonal antibody (MAB) like 4BE12C10, H44/24, H44/58, H44/70 or
XX H44/78. (I) is antigenically cross-reactive with MAB. (I) have
XX antibacterial and antiinflammatory activities, and can be used in
XX vaccines. MAB is useful in the identification of (I). (I) or MAB are
XX useful as a medicament, and also in the manufacture of a medicament for
XX treating or preventing meningococcal disease. (I) and MAB are useful for
XX treating a patient suffering from or susceptible to meningococcal disease
XX by administering (I) or MAB to the patient. (I) is useful in a diagnostic
XX assay for meningococcal infection to detect antibodies against L3, 7, 9,
XX LOS and to detect the presence of L3, 7, 9 immunotype meningococcus in a
XX sample from a patient. ABN88464 to ABN88487 and ABP47336 to ABP47754
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 11 AA;
XX
XX Query Match 47.5%; Score 29; DB 5; Length 11;
XX Best Local Similarity 27.3%; Pred. No. 3.1e+02;
XX Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 CTSVPLTSVPC 11
XX |::|
XX 1 CWTIPYRGTC 11
XX
XX Db
XX
XX RESULT 15
XX AAR77368
XX ID AAR77368 standard; peptide; 10 AA.
XX
XX AC AAR77368;
XX
XX 17-JAN-1996 (first entry)
XX
XX SH3 binding domain CAIR-1 B.
XX
XX Carboxyamido-triazole resistance; CAI; CAIR-1; cancer; gene therapy;
XX Src homology 3; SH3 binding domain.
XX
XX Homo sapiens.
XX
XX WO9525125-A1.
XX
XX 21-SEP-1995.
XX
XX 14-MAR-1995; 95WO-US0003610.
XX
XX 14-MAR-1994; 94US-00212190.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Kohn EC, Liotta LA, Kim YS;
XX WPI; 1995-336944/43.
XX
XX DNA encoding CAI resistance proteins - used in gene therapy, and for
XX detecting CAI resistance in biological samples.

```

PS Example 4; Page 40; 56pp; English.
XX
CC CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058 human
CC melanoma cells, contains a unique proline-rich sequence which fulfills
CC the consensus definition for Src homology 3 (SH3) binding proteins
CC (AAR77366). 4 Unique versions (AAR77367-70) are present
XX
SQ Sequence 10 AA;
Query Match 44.3%; Score 27; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 VPLTSVPC 11
Db 1 VPPAPVPC 8

Search completed: September 5, 2004, 10:46:32
Job time : 66 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:46:55 ; Search time 67 Seconds
(without alignments)
51.727 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 171292

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
12: /cgn2_6/ptodata/2/pubpaa/US09D_NEW_PUB.pcp.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_NEW_PUB.pcp.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	61	100.0	11	9	US-09-761-636A-7	Sequence 7, Appl
2	59	96.7	11	9	US-09-761-636A-23	Sequence 23, Appl
3	57	93.4	11	9	US-09-761-636A-26	Sequence 26, Appl
4	54	88.5	11	9	US-09-761-636A-24	Sequence 24, Appl
5	52	85.2	11	9	US-09-761-636A-25	Sequence 25, Appl
6	45.5	74.6	10	9	US-09-761-636A-13	Sequence 13, Appl
7	41	67.2	9	9	US-09-761-636A-14	Sequence 14, Appl
8	32	52.5	9	9	US-09-761-636A-10	Sequence 10, Appl
9	29	47.5	9	12	US-10-253-876-332	Sequence 332, App
10	29	47.5	9	15	US-10-245-871-332	Sequence 332, App
11	29	47.5	11	12	US-10-398-104-155	Sequence 155, App
12	29	47.5	11	12	US-10-398-104-156	Sequence 156, App
13	29	47.5	11	14	US-10-126-845-89	Sequence 89, Appl
14	28	45.9	9	15	US-10-154-884B-11221	Sequence 11221, A
15	27	44.3	9	15	US-10-154-884B-11228	Sequence 11228, A

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16 27 44.3 9 15 US-10-154-884B-11250  Sequence 11250, A
17 27 44.3 9 15 US-10-154-884B-11254  Sequence 11254, A
18 27 44.3 9 15 US-10-154-884B-11258  Sequence 11258, A
19 27 44.3 9 15 US-10-154-884B-11259  Sequence 11259, A
20 27 44.3 9 15 US-10-154-884B-11265  Sequence 11265, A
21 27 44.3 9 15 US-10-154-884B-11275  Sequence 11275, A
22 27 44.3 9 15 US-10-154-884B-11280  Sequence 11280, A
23 27 44.3 11 12 US-10-398-104-172  Sequence 172, App
24 26 42.6 9 13 US-10-066-151-20  Sequence 20, Appl
25 26 42.6 9 13 US-10-358-052-20  Sequence 20, Appl
26 26 42.6 10 11 US-09-833-245-1011  Sequence 1011, Ap
27 25 41.0 9 13 US-10-066-151-19  Sequence 19, Appl
28 25 41.0 9 15 US-10-358-052-19  Sequence 19, Appl
29 25 41.0 9 15 US-10-358-052-52  Sequence 52, Appl
30 25 41.0 9 16 US-10-471-895-10  Sequence 10, Appl
31 25 41.0 10 10 US-09-572-404B-2047  Sequence 2047, Ap
32 25 41.0 11 14 US-10-126-845-12  Sequence 12, Appl
33 25 41.0 11 14 US-10-126-845-70  Sequence 70, Appl
34 25 41.0 11 15 US-10-116-275-100  Sequence 100, App
35 25 41.0 11 16 US-10-784-235-12  Sequence 12, Appl
36 24 39.3 5 9 US-09-886-135-5  Sequence 5, Appl
37 24 39.3 5 10 US-09-886-135-5  Sequence 5, Appl
38 24 39.3 7 9 US-09-761-636A-11  Sequence 11, Appl
39 24 39.3 7 12 US-10-620-278-19  Sequence 19, Appl
40 24 39.3 7 14 US-10-220-033-28  Sequence 28, Appl
41 24 39.3 9 12 US-09-935-430-249  Sequence 249, App
42 24 39.3 9 12 US-09-935-430-322  Sequence 322, App
43 24 39.3 9 12 US-09-935-430-349  Sequence 349, App
44 24 39.3 9 12 US-09-935-430-464  Sequence 464, App
45 24 39.3 9 13 US-10-066-151-21  Sequence 21, Appl

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ALIGNMENTS

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RESULT 1
US-09-761-636A-7
; Sequence 7, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761.636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-7

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Query Match      100.0%; Score 61; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CISVPLTSVPC 11
        |||
Db      1 CISVPLTSVPC 11

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RESULT 2
US-09-761-636A-23
; Sequence 23, Application US/09761636A
; Patent No. US20020065218A1

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GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US 09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 23
; TYPE: PRT
; LENGTH: 11
; ORGANISM: synthetic construct
US-09-761-636A-23

Query Match 96.7%; Score 59; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0074; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPLTSVPC 11
Db 1 CUSVPLTSVPC 11

RESULT 3
US-09-761-636A-26
; Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-26

Query Match 93.4%; Score 57; DB 9; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.015; Mismatches 2; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPLTSVPC 11
Db 1 CUSVPLTSVPC 11

RESULT 4
US-09-761-636A-24
; Sequence 24, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
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; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-24

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Best Local Similarity 72.7%; Pred. No. 0.046; Mismatches 3; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPLTSVPC 11
Db 1 CUSVPLTSVPC 11

RESULT 5
US-09-761-636A-25
; Sequence 25, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25

Query Match 85.2%; Score 52; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.095; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CUSVPLTSVPC 11
Db 1 CUSVPLTSVPC 11

RESULT 6
US-09-761-636A-13
; Sequence 13, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293


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; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match      74.6%; Score 45.5; DB 9; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.93;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPLTSVPC 11
Db 1 CISVPL-SVPC 10

RESULT 7
US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-14

Query Match      67.2%; Score 41; DB 9; Length 9;
Best Local Similarity 81.8%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 CISVPLTSVPC 11
Db 1 CISVPL--VPC 9

RESULT 8
US-09-761-636A-10
; Sequence 10, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-10

Query Match      52.5%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
Db 2 SVPLTSV 8

RESULT 9
US-10-253-286-332
; Sequence 332, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-332

Query Match      47.5%; Score 29; DB 12; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLTSVP 10
Db 2 VPIITSP 8

RESULT 10
US-10-245-871-332
; Sequence 332, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-332

Query Match      47.5%; Score 29; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Query Match	47.5%	Score 29	DB 12	Length 11
Best Local Similarity	36.4%	Pred. No. 4.2e+02		
Matches	4	Conservative	2	Mismatches 5; Indels 0; Gaps 0
QY	1	CISVPLTSVPC 11		
Db	1	CFAPPYDPLPC 11		
RESULT 13				
US-10-126-845-89				
Sequence 89, Application US/10126845				
Publication No. US20030181367A1				
GENERAL INFORMATION:				
APPLICANT: O'Mahony, Daniel J.				
APPLICANT: Lambkin, Imelda J.				
APPLICANT: Pinilla, Clemencia				
APPLICANT: Houghten, Richard				
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM				
FILE REFERENCE: E1067/20058				
CURRENT APPLICATION NUMBER: US/10/126,845				
CURRENT FILING DATE: 2002-10-15				
NUMBER OF SEQ ID NOS: 119				
SOFTWARE: PatentIn version 3.1				
SEQ ID NO 89				
LENGTH: 11				
TYPE: PRT				
ORGANISM: Artificial Sequence				
FEATURE:				
OTHER INFORMATION: D form peptide				
FEATURE:				
NAME/KEY: MISC FEATURE				
LOCATION: (1)-(11)				
OTHER INFORMATION: D form retroinversion peptide				
US-10-126-845-89				
Query Match	47.5%	Score 29	DB 14	Length 11
Best Local Similarity	45.5%	Pred. No. 4.2e+02		
Matches	5	Conservative	1	Mismatches 5; Indels 0; Gaps 0
QY	1	CISVPLTSVPC 11		
Db	1	CLLVPLLVAC 11		
RESULT 14				
US-10-154-884B-11221				
Sequence 11221, Application US/10154884B				
Publication No. US20040005561A1				
GENERAL INFORMATION:				
APPLICANT: Gaiger, Alexander				
APPLICANT: Algate, Paul A.				
APPLICANT: Mannion, Jane				
APPLICANT: Retter, Marc W.				
APPLICANT: Corixa Corporation				
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and				
TITLE OF INVENTION: Hematological Malignancies				
FILE REFERENCE: 014058-013521US				
CURRENT APPLICATION NUMBER: US/10/154,884B				
CURRENT FILING DATE: 2002-05-23				
PRIOR FILING DATE: 2000-03-01				
PRIOR APPLICATION NUMBER: US 60/186,126				
PRIOR FILING DATE: 2000-03-01				
PRIOR APPLICATION NUMBER: US 60/190,479				
PRIOR FILING DATE: 2000-03-17				
PRIOR APPLICATION NUMBER: US 60/200,545				
PRIOR FILING DATE: 2000-04-27				
PRIOR APPLICATION NUMBER: US 60/200,303				
PRIOR FILING DATE: 2000-04-28				
PRIOR APPLICATION NUMBER: US 60/200,779				
PRIOR FILING DATE: 2000-04-28				
PRIOR APPLICATION NUMBER: US 60/200,999				
PRIOR FILING DATE: 2000-05-01				
PRIOR APPLICATION NUMBER: US 60/202,084				

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; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11221

Query Match          45.9%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPL 7
Db 2 CLSVFVS 8

RESULT 15
US-10-154-884B-11228
; Sequence 11228, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11228
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11228

Query Match          44.3%; Score 27; DB 15; Length 9;
Best Local Similarity 56.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CUSVPL 6
Db 4 CLSVFVS 9
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uspto

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:45:30 ; Search time 20 Seconds
(without alignments)
28.394 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 112282

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	49.2	8	1 US-08-189-331-150	Sequence 150, App
2	30	49.2	8	2 US-08-471-068-150	Sequence 150, App
3	27	44.3	10	1 US-08-212-190A-5	Sequence 5, Appl
4	27	44.3	10	2 US-08-900-321-5	Sequence 5, Appl
5	27	44.3	10	5 PCT-US95-03610-5	Sequence 5, Appl
6	26	42.6	6	2 US-08-769-745-15	Sequence 15, Appl
7	26	42.6	8	1 US-08-189-331-149	Sequence 149, App
8	26	42.6	8	2 US-08-471-068-149	Sequence 149, App
9	25.5	41.8	9	1 US-08-331-383-33	Sequence 33, Appl
10	25.5	41.8	9	1 US-08-549-008-43	Sequence 43, Appl
11	25.5	41.8	9	3 US-08-802-981-143	Sequence 143, App
12	25	41.0	8	1 US-08-360-239B-1	Sequence 1, Appl
13	25	41.0	10	2 US-08-483-077C-26	Sequence 26, Appl
14	25	41.0	10	2 US-08-519-109B-26	Sequence 26, Appl
15	25	41.0	10	2 US-08-482-228-108	Sequence 108, App
16	25	41.0	10	3 US-08-482-528-108	Sequence 108, App
17	25	41.0	10	5 PCT-US95-10811-38	Sequence 38, Appl
18	24	39.3	6	1 US-08-483-434A-21	Sequence 21, Appl
19	24	39.3	6	3 US-08-476-134A-30	Sequence 30, Appl
20	24	39.3	6	6 5190920-26	Patent No. 5190920
21	24	39.3	6	6 5506208-28	Patent No. 5506208
22	24	39.3	7	4 US-09-438-150-1	Sequence 1, Appl
23	24	39.3	9	2 US-08-340-283-154	Sequence 154, App
24	24	39.3	9	4 US-09-601-729-204	Sequence 204, App
25	24	39.3	10	3 US-08-836-075A-187	Sequence 187, App
26	23.5	38.5	9	1 US-08-331-383-31	Sequence 31, Appl
27	23.5	38.5	9	1 US-08-549-008-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-189-331-150
; Sequence 150, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-189-331-150

Query Match 49.2%; Score 30; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CISVPLTS 8
Db 1 CVSAFQTS 8

28	23.5	38.5	9	3	US-08-802-981-142	Sequence 142, App
29	23.5	38.5	11	3	US-08-802-981-144	Sequence 144, App
30	23	37.7	8	1	US-08-189-331-147	Sequence 147, App
31	23	37.7	8	1	US-08-189-331-148	Sequence 148, App
32	23	37.7	8	2	US-08-340-283-61	Sequence 61, Appl
33	23	37.7	8	2	US-08-471-068-147	Sequence 147, App
34	23	37.7	8	2	US-08-471-068-148	Sequence 148, App
35	23	37.7	9	1	US-08-193-075-4	Sequence 4, Appl
36	23	37.7	9	1	US-08-467-083-3	Sequence 3, Appl
37	23	37.7	9	1	US-08-414-417B-3	Sequence 3, Appl
38	23	37.7	9	2	US-08-486-348A-3	Sequence 3, Appl
39	23	37.7	9	2	US-08-468-545B-3	Sequence 3, Appl
40	23	37.7	9	3	US-08-466-680B-3	Sequence 3, Appl
41	23	37.7	9	4	US-08-403-459-25	Sequence 25, Appl
42	23	37.7	9	4	US-09-997-579-19	Sequence 19, Appl
43	23	37.7	9	4	US-09-354-533-3	Sequence 3, Appl
44	23	37.7	9	5	PCT-US95-01672-4	Sequence 4, Appl
45	23	37.7	10	1	US-08-033-857A-5	Sequence 5, Appl

RESULT 2
US-08-471-068-150
; Sequence 150, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-150
Query Match 49.2%; Score 30; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTSVPLTS 8
Db 1 CVSAPQTS 8
RESULT 3
US-08-212-190A-5
; Sequence 5, Application US/08212190A
; Patent No. 5652223
; GENERAL INFORMATION:
; APPLICANT: KOHN, Elise C.
; APPLICANT: LIOTTA, Lance A.
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,190A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 15280-204US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-212-190A-5
Query Match 44.3%; Score 27; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 VPLTSVPC 11
Db 1 VPPAPVPC 8
RESULT 4
US-08-900-321-5
; Sequence 5, Application US/08900321
; Patent No. 5981712
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-900-321-5

Query Match 44.3%; Score 27; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLTSVPC 11
|||
Db 1 VPPAPVPC 8

RESULT 5
PCT-US95-03610-5
; Sequence 5, Application PC/TUS9503610
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; TITLE OF INVENTION: US95 THEROP
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03610
; FILING DATE: 14-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-204000PC
; REFERENCE/DOCKET NUMBER: DHHS Ref. No. E-112-94/0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-03610-5

Query Match 44.3%; Score 27; DB 5; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLTSVPC 11
|||
Db 1 VPPAPVPC 8

RESULT 6
US-08-769-745-15
; Sequence 15, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Holmes, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; CHANNEL ACTIVITY

; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-15

Query Match 42.6%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSVP 10
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Db 1 PLTPVP 6

RESULT 7
US-08-189-331-149
; Sequence 149, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-189-331-149

Query Match 42.6%; Score 26; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLT 7
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Db 2 CVSAPQT 8

RESULT 8
US-08-471-068-149

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/ Sequence 149, Application US/08471068
/ Patent No. 5948635
/ GENERAL INFORMATION:
/ APPLICANT: Kay, B. K.
/ APPLICANT: Fowkes, D. M.
/ TITLE OF INVENTION: Totally Synthetic Affinity Reagents
/ NUMBER OF SEQUENCES: 186
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/471,068
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/189,331
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mirock, S. Lealie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-155
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 790-9090
/ TELEFAX: 212 869-8864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 149:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ PS-08-471-068-149

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Query Match	42.6%;	Score 26;	DB 2;	Length 8;
Best Local Similarity	57.1%;	Pred. No. 3+05;		
Matches 4:	Conservative	1;	Mismatches	2;
			Indels	0;
			Gaps	0;

Qy	1	CISVPLT	7
		:	
Dp	2	CVSAPOT	8

RESULT 9
US-08-331-383-33
; Sequence 33, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Processes in Biological Samples and Methods and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.25
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, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/331.383
, FILING DATE: 28-OCT-1994
, CLASSIFICATION: 424
, ATTORNEY/AGENT INFORMATION:
, NAME: Dow, Karen B.
, REGISTRATION NUMBER: 29,684
, REFERENCE/DOCKET NUMBER: 16865-1
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 415-326-2400
, TELEFAX: 415-326-2422
, INFORMATION FOR SEQ ID NO: 33:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 9 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: peptide
, US-08-331-383-33

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Query Match	41.8%	Score 25.5;	DB 1;	Length 9;
Best Local Similarity	44.4%;	Pred. No. 3e+05;		
Matches	4;	Conservative	4;	Mismatches 0;
		Indels	1;	Gaps 1;

Qy	3	SVPLTSVPC	11
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Db	2	AIPM-SIPC	9

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; MOLECULE TYPE: peptide
US-08-549-008-43
Query Match 41.8%; Score 25.5; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 3 SVPLTSVPC 11
DB 2 AIPM-SIPC 9

RESULT 11
US-08-802-981-143
; Sequence 143, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-143
Query Match 41.8%; Score 25.5; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 3 SVPLTSVPC 11
DB 2 AIPM-SIPC 9

RESULT 12
US-08-360-239B-1
; Sequence 1, Application US/08360239B
; Patent No. 5801222
; GENERAL INFORMATION:
; APPLICANT: Pettit, George R.
; APPLICANT: Tan, Rui
; TITLE OF INVENTION: Isolation and Structure of
; TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic
; TITLE OF INVENTION: Octapeptides Phakellistatin 10 and 11

; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Mybeck
; STREET: 8010 East Morgan Trail, #10
; CITY: Scottsdale
; STATE: Arizona
; COUNTRY: USA
; ZIP: 85258-1234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,239B
; FILING DATE: 12/20/94
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard R. Mybeck
; REGISTRATION NUMBER: 17,886
; REFERENCE/DOCKET NUMBER: 4997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (602)-483-1285
; TELEFAX: (602)-483-7452
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; TOPOLOGY: Cyclic
; MOLECULE TYPE:
; DESCRIPTION: Cyclooctapeptide
; DESCRIPTION: phakellistatin 10
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: circular
; ORIGINAL SOURCE:
; ORGANISM: Phakellia sp.
; DEVELOPMENTAL STAGE: whole organism
; FEATURE:
; NAME/KEY: Phakellistatin 10
; NAME/KEY: amino acid analysis, high resolution
; NAME/KEY: nuclear magnetic resonance and mass
; NAME/KEY: spectral MS/MS techniques
; OTHER INFORMATION: Phakellistatin 10 is a
; OTHER INFORMATION: cell growth inhibitory peptide with
; OTHER INFORMATION: activity in murine lymphocytic leukemia
; OTHER INFORMATION: cell line of 2.1 mg/ml.
US-08-360-239B-1
Query Match 41.0%; Score 25; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 1 PLTPIP 6

RESULT 13
US-08-483-077C-26
; Sequence 26, Application US/08483077C
; Patent No. 5811391
; GENERAL INFORMATION:
; APPLICANT: Arthenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; TITLE OF INVENTION: Compositions and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
```

CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,077C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CY 1647
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 10
OTHER INFORMATION: /note= "The carboxy-terminus is a carboxamide."
US-08-519-109B-26

Query Match 41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISVPLTSP 10
Db 2 LDVPILDVP 10

RESULT 15
US-08-482-228-108
Sequence 108, Application US/08482228
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE RELEASE
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
US-08-482-228-108

Query Match 41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 56.7%; Pred. No. 3.4e+02;

CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,077C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CY 1647
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 10
OTHER INFORMATION: /note= "The carboxy-terminus is a carboxamide."
US-08-483-077C-26

Query Match 41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISVPLTSP 10
Db 2 LDVPILDVP 10

RESULT 14
US-08-519-109B-26
Sequence 26, Application US/08519109B
Patent No. 5869448
GENERAL INFORMATION:
APPLICANT: Arthenius, Thomas S.
APPLICANT: Tempczyk, Anna
APPLICANT: Elices, Mariano J.
APPLICANT: Zheng, Zhong-Li
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics.
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,109B
FILING DATE: 25-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLTSV 9
 |||
Db 2 CIDVFLTCV 10

Search completed: September 5, 2004, 10:48:51
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:52:56 ; Search time 21 Seconds
(without alignments)
77.869 Million cell updates/sec

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCRPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2990

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	34.0	16	2	PH1477
2	33.5	33.5	12	2	PT0216
3	32	32.0	16	2	PH1472
4	32	32.0	16	2	PH1473
5	32	32.0	16	2	PH1480
6	30	30.0	12	2	S47394
7	29.5	29.5	13	2	S47357
8	29	29.0	12	2	S26549
9	29	29.0	14	2	G44957
10	29	29.0	17	2	C24166
11	28	28.0	12	2	PH1463
12	28	28.0	12	2	PH1466
13	28	28.0	13	2	S47400
14	28	28.0	16	2	PH1474
15	27	27.0	11	2	PT0217
16	27	27.0	12	2	S47391
17	27	27.0	13	2	S47383
18	27	27.0	14	2	PA0013
19	27	27.0	16	2	PH1476
20	27	27.0	17	2	S57519
21	26	26.0	11	2	S57575
22	26	26.0	12	2	S47395
23	26	26.0	13	2	S47381
24	26	26.0	15	2	B49655
25	25.5	25.5	13	2	S47382
26	25.5	25.5	15	2	PH0752
27	25.5	25.5	15	2	PH0760
28	25	25.0	10	2	S23371
29	25	25.0	11	2	PH0947

30 25 25.0 12 2 PH1469 T-cell receptor be
31 25 25.0 12 2 PH0931 T-cell receptor be
32 25 25.0 14 2 PH0753 T-cell receptor be
33 25 25.0 15 2 PH0808 T-cell receptor al
34 25 25.0 17 2 C49255 T-cell receptor be
35 24.5 24.5 12 2 PH1457 T-cell receptor be
36 24 24.0 11 2 PH1583 T-cell receptor be
37 24 24.0 12 2 S26552 T-cell receptor be
38 24 24.0 12 2 S26559 T-cell receptor be
39 24 24.0 12 2 S26554 T-cell receptor be
40 24 24.0 12 2 S47363 T-cell receptor be
41 24 24.0 12 2 PH1467 T-cell antigen rec
42 24 24.0 12 2 PH1468 T-cell receptor be
43 24 24.0 13 2 A28953 alpha-conotoxin SI
44 24 24.0 13 2 S47390 T-cell antigen rec
45 24 24.0 15 1 NTKNAG alpha-conotoxin GI

ALIGNMENTS

RESULT 1

PH1477

T-cell receptor beta chain (clone A3/H2R5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995

C:Accession: PH1477

R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko J. Exp. Med. 177, 811-820, 1993

A>Title: T cell receptor selection by and recognition of two class I major histocompatib

A:Reference number: PH1430; MUID:93171821; PMID:8436911

A:Accession: PH1477

A:Molecule type: mRNA

A:Residues: 1-16 <CAS>

A:Experimental source: cytolytic T-lymphocyte

C:Superfamily: immunoglobulin homology

C:Keywords: receptor; T-cell

Query Match 34.0%; Score 34; DB 2; Length 16;

Best Local Similarity 60.0%; Pred. No. 70;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CASELGKSTN 10

Db 1 CASSVGTGTN 10

RESULT 2

PT0216

T-cell receptor beta chain V-J region (4-1-G.4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C:Accession: PT0216

R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A>Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric

A:Reference number: PT0209; MUID:91217621; PMID:1902501

A:Accession: PT0216

A:Molecule type: mRNA

A:Residues: 1-12 <NAK>

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 33.5%; Score 33.5; DB 2; Length 12;

Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CASELGKSTNT 11

Db 1 CASSLG-TTNT 10

RESULT 3

PH1472

T-cell receptor beta chain (clone A24/12.2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C:Accession: PH1472
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
 J. Exp. Med. 177, 811-820, 1993
 A:Title: T cell receptor selection by and recognition of two class I major histocompatib
 A:Reference number: PH1430; MUID:93171821; PMID:8436911
 A:Accession: PH1472
 A:Molecule type: mRNA
 A:Residues: 1-16 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 32.0%; Score 32; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTN 10
 ||| |||
 DB 1 CASSLGTGNN 10

RESULT 4
 PH1473
 T-cell receptor beta chain (clone A3/IIIC5) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C:Accession: PH1473
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
 J. Exp. Med. 177, 811-820, 1993
 A:Title: T cell receptor selection by and recognition of two class I major histocompatib
 A:Reference number: PH1430; MUID:93171821; PMID:8436911
 A:Accession: PH1473
 A:Molecule type: mRNA
 A:Residues: 1-16 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 32.0%; Score 32; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTN 10
 ||| |||
 DB 1 CASSYGTGIN 10

RESULT 5
 PH1480
 T-cell receptor beta chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 27-Oct-1995
 C:Accession: PH1480; PH1478
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
 J. Exp. Med. 177, 811-820, 1993
 A:Title: T cell receptor selection by and recognition of two class I major histocompatib
 A:Reference number: PH1430; MUID:93171821; PMID:8436911
 A:Accession: PH1480
 A:Molecule type: mRNA
 A:Residues: 1-16 <CAS1>
 A:Experimental source: cytolytic T-lymphocyte, clone A3/C80b
 A:Accession: PH1478
 A:Molecule type: mRNA
 A:Residues: 1-16 <CAS2>
 A:Experimental source: cytolytic T-lymphocyte, clone A24/PEF5
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 32.0%; Score 32; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CASELGKSTN 10
 ||| |||
 DB 1 CASSTGTGTN 10

RESULT 6

S47394
 T-cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S47394; S47369
 R:Lehner, P.J.
 submitted to the EMBL Data Library, August 1994
 A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
 A:Reference number: S47355
 A:Accession: S47394
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-12 <LEH>
 A:Cross-references: EMBL:Z35714; NID:g527523; PIDN:CAA84783.1; PID:g527524; EMBL:Z35694;
 C:Keywords: T-cell receptor

Query Match 30.0%; Score 30; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
 ||| : |||
 DB 1 CASSIGNGYTF 12

RESULT 7

S47357
 T-cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S47357
 R:Lehner, P.J.
 submitted to the EMBL Data Library, August 1994
 A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
 A:Reference number: S47355
 A:Accession: S47357
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:Z35691; NID:g527451; PIDN:CAA84750.1; PID:g527452
 C:Keywords: T-cell receptor

Query Match 29.5%; Score 29.5; DB 2; Length 13;
 Best Local Similarity 63.6%; Pred. No. 2.9e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
 ||| : |||
 DB 1 CASS-GRSTDT 10

RESULT 8

S26549
 T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 C:Accession: S26549; S26550
 R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi
 J. Exp. Med. 176, 439-447, 1992
 A:Title: H-2 restricted cytolytic T lymphocytes specific for HLA display T cell recepto
 A:Reference number: S26512; MUID:92364546; PMID:1380061
 A:Accession: S26549
 A:Molecule type: mRNA
 A:Residues: 1-12 <CAS>
 A:Cross-references: EMBL:X67999

A;Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
 A;Accession: S26550
 A;Molecule type: mRNA
 A;Residues: 1-12 <CA2>
 A;Cross-references: EMBL:X68000
 A;Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: T-cell receptor

Query Match 29.0%; Score 29; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 3.3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGKS 8
 ||| |||:
 Db 1 CASSLGET 8

RESULT 9
 G44957
 photosystem II oxygen-evolving complex protein 2 - common tobacco (cv. Samsun NN) (fragm
 C;Species: Nicotiana tabacum (common tobacco)
 C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Jun-1993
 C;Accession: G44957
 R;Akeda, S.; Sato, F.; Ida, K.; Yamada, Y.
 Plant Cell Physiol. 31, 215-221, 1990
 A;Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum
 A;Reference number: A44957
 A;Accession: G44957
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <TAK>

Query Match 29.0%; Score 29; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3.7e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GKSTNTFCCK 15
 ||| |||:
 Db 3 GEAAVFGKP 12

RESULT 10
 C24166
 photosystem II extrinsic membrane protein - spinach (fragment)
 C;Species: Spinacia oleracea (spinach)
 C;Date: 05-Jun-1987 #sequence_revision 21-May-1988 #text_change 24-Apr-1998
 C;Accession: C24166
 R;Vater, J.; Sainikow, J.; Jansson, C.
 FEBS Lett. 203, 230-234, 1986
 A;Title: N-terminal sequence determination and secondary structure analysis of extrinsic
 A;Reference number: A24166
 A;Accession: C24166
 A;Molecule type: protein
 A;Residues: 1-17 <VAI>
 C;Superfamily: photosystem II oxygen-evolving complex protein 2
 C;Keywords: chloroplast; membrane protein; thylakoid

Query Match 29.0%; Score 29; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 4.4e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GKSTNTFCCK 15
 ||| |||:
 Db 2 GEAAVFGKP 11

RESULT 11
 PH1463
 T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C;Accession: PH1463

R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
 J. Exp. Med. 177, 811-820, 1993
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib
 A;Reference number: PH1430; MUID:93171821; PMID:8436911
 A;Accession: PH1463
 A;Molecule type: mRNA
 A;Residues: 1-12 <CAS>
 A;Experimental source: cytolytic T-lymphocyte
 C;Superfamily: immunoglobulin homology
 C;Keywords: receptor; T-cell

Query Match 28.0%; Score 28; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 4.7e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKS 8
 ||| |||:
 Db 1 CASSLGNT 8

RESULT 12
 PH1466
 T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C;Accession: PH1466
 R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
 J. Exp. Med. 177, 811-820, 1993
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib
 A;Reference number: PH1430; MUID:93171821; PMID:8436911
 A;Accession: PH1466
 A;Molecule type: mRNA
 A;Residues: 1-12 <CAS>
 A;Experimental source: cytolytic T-lymphocyte
 C;Superfamily: immunoglobulin homology
 C;Keywords: receptor; T-cell

Query Match 28.0%; Score 28; DB 2; Length 12;
 Best Local Similarity 71.4%; Pred. No. 4.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7
 ||| |||:
 Db 1 CASSLGQ 7

RESULT 13
 S47400
 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47400
 R;Löhner, P.J.
 submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
 A;Reference number: S47355
 A;Accession: S47400
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <LEH>
 A;Cross-references: EMBL:Z35678; NID:g527535; PIDN:CAA84747.1; PID:g527536
 C;Keywords: T-cell receptor

Query Match 28.0%; Score 28; DB 2; Length 13;
 Best Local Similarity 41.7%; Pred. No. 5e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTP 12
 ||| |||:
 Db 1 CASSVALATEAF 12

RESULT 14

PH1474
T-cell receptor beta chain (clone A2/25) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1474
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:9436911
A:Accession: PH1474
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 28.0%; Score 28; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CASELGKSTN 10
DB 1 CASSPGTGNN 10

RESULT 15
PT0217
T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0217
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0217
A:Molecule type: mRNA
A:Residues: 1-11 <NAK>
C:Keywords: T-cell receptor

Query Match 27.0%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CASELG 6
DB 1 CASRLG 6

Search completed: September 5, 2004, 10:56:30
Job time : 21 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:48:56 ; Search time 15 Seconds
(without alignments)
59.013 Million cell updates/sec

Title: US-09-761-636A-8
Perfect score: 100
Sequence: 1 CASELGKSTNTFCPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 943

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	27	27.0	14	1	CX1A_CONBE
2	26	26.0	12	1	PSP3_PHYPA
3	25.5	25.5	15	1	UC19_MAIZE
4	24	24.0	15	1	CX1A_CONGE
5	23	23.0	13	1	CX1A_CONGE
6	23	23.0	13	1	CX1A_CONGE
7	23	23.0	13	1	CX1A_CONGE
8	23	23.0	13	1	CX1A_CONGE
9	23	23.0	14	1	CX1A_CONGE
10	23	23.0	15	1	CX1B_CONBE
11	23	23.0	15	1	CX1B_CONBE
12	23	23.0	16	1	CX1A_CONAL
13	23	23.0	16	1	CX1A_CONAL
14	23	23.0	16	1	CX1A_CONAL
15	23	23.0	16	1	CX1A_CONAL
16	22	22.0	15	1	ARCA_STRP5
17	22	22.0	15	1	ARCA_STRP5
18	22	22.0	15	1	ARCA_STRP5
19	21	21.0	12	1	CX1A_CONBE
20	21	21.0	12	1	CX1A_CONBE
21	20	20.0	12	1	UC19_MAIZE
22	20	20.0	12	1	UC19_MAIZE
23	20	20.0	12	1	UC19_MAIZE
24	20	20.0	12	1	UC19_MAIZE
25	19	19.0	7	1	TPFY_PACDA
26	19	19.0	7	1	TPFY_PACDA
27	19	19.0	10	1	COXM_RAT
28	19	19.0	11	1	CX5A_CONAL
29	19	19.0	11	1	CX5B_CONAL
30	19	19.0	12	1	PAR7_PENNO
31	19	19.0	13	1	FAR7_PENNO
32	19	19.0	15	1	CX3A_CONQU
33	19	19.0	15	1	CX3B_CONQU

34 18 18.0 12 1 UR2B_CYPCA
35 18 18.0 15 1 MUP_CAYPO
36 17 17.0 9 1 COW_CONVE
37 17 17.0 15 1 C10A_RAT
38 17 17.0 15 1 CH11_PEA
39 17 17.0 15 1 ONC1_ONCMY
40 17 17.0 16 1 AHI_FRUSE
41 17 17.0 16 1 CERB_RAT
42 17 17.0 16 1 KTRC_AREMA
43 17 17.0 17 1 BOL1_MEGPE
44 17 17.0 17 1 BOL2_MEGPE
45 17 17.0 17 1 BOL3_MEGPE

ALIGNMENTS

RESULT 1
CX1A_CONBE STANDARD; PRT; 14 AA.
AC P58623;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Conotoxin BetXia.
OS Conus betulinus (Beech cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbecoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89764;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20058566; PubMed=10591037;
RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
RT "Studies on conotoxins of Conus betulinus.";
RL J. Nat. Toxins 8:341-349 (1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1589.3; METHOD=MALDI.
KW Neurotoxin; Toxin.
FT DISULFID 1 9 PROBABLE.
FT DISULFID 2 12 PROBABLE.
FT DISULFID 6 13 PROBABLE.
SQ SEQUENCE 14 AA; 1597 MW; 95B725AA93432EB1 CRC64;
Query Match 27.0%; Score 27; DB 1; Length 14;
Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 7 KSTNTFCPPC 17
Db 3 KQSCCTCPC 13
RESULT 2
PSP3_PHYPA STANDARD; PRT; 12 AA.
AC P80662;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OE2) (24 kDa subunit of oxygen evolving system of photosystem II) (Fragment).
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;

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RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RL plastid enzymes.";
RL Planta 201:261-272(1997).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex.
CC -!- INDUCTION: By light.
CC -!- SIMILARITY: Belongs to the psbP family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
KW Multigene family.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C44DC5 CRC64;

Query Match 26.0%; Score 26; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GKSTNTEFCVP 15
|:|:|:|:|
Db 3 GESANVFQAP 12

RESULT 3
UC19 MAIZE STANDARD; PRT; 15 AA.
AC P80625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 406)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.6, its MW is: 18.4 kDa.
DR Maize-2DPAGE; P80625; COLEOPTILE.
DR MaizeDB; 123951; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1672 MW; 1CF69D4DA8737F9D CRC64;

Query Match 25.5%; Score 25.5; DB 1; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 6 GKSTNTEFCVP 16
|:|:|:|:|
Db 2 GRRVTTGCSPP 13

RESULT 4
CXAL CONGE STANDARD; PRT; 15 AA.
AC P01579;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-conotoxin GIA [contains: Alpha-conotoxin GI (GI)].
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;

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OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RA MEDLINE=81191854; PubMed=7014556;
RA Gray W.R., Luque F.A., Olivera B.M., Barrett J., Cruz L.J.;
RT "Peptide toxins from Conus geographus venom.";
RL J. Biol. Chem. 256:4734-4740(1981).
RN [2]
RP DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.
RP MEDLINE=83105694; PubMed=7152021;
RA Nishiuchi Y., Sakakibara S.;
RT "Primary and secondary structure of conotoxin GI, a neurotoxic
RT tridecapeptide from a marine snail.";
RL FEBS Lett. 148:260-262(1982).
RN [3]
RP DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.
RP MEDLINE=84280842; PubMed=6466616;
RA Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,
RA Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
RA Cruz L.J., Rivier J.;
RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of
RT iodinated derivatives.";
RL Biochemistry 23:2796-2802(1984).
RN [4]
RP COMPARISON WITH ALPHA-CONOTOXIN SI AND ALPHA-CONOTOXIN MI.
RP MEDLINE=95034849; PubMed=7947815;
RA Hann R.M., Pagan O.R., Sterovic V.A.;
RT "The alpha-conotoxins GI and MI distinguish between the nicotinic
RT acetylcholine receptor agonist sites while SI does not.";
RL Biochemistry 33:14058-14063(1994).
RN [5]
RP PHARMACOLOGICAL CHARACTERIZATION ON MOUSE MUSCLE-DERIVED BC3H-1 CELLS
RP AND TORPEDO ELECTRIC ORGAN.
RP MEDLINE=95349531; PubMed=7623764;
RA Groebe D.R., Dumm J.M., Levitan E.S., Abramson S.N.;
RT "alpha-Conotoxins selectively inhibit one of the two acetylcholine
RT binding sites of nicotinic receptors.";
RL Mol. Pharmacol. 48:105-111(1995).
RN [6]
RP MUTAGENESIS OF ARG-9.
RP MEDLINE=97317090; PubMed=9174364;
RA Groebe D.R., Gray W.R., Abramson S.N.;
RT "Determinants involved in the affinity of alpha-conotoxins GI and SI
RT for the muscle subtype of nicotinic acetylcholine receptors.";
RL Biochemistry 36:6469-6474(1997).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.2 ANGSTROMS) OF GI.
RP MEDLINE=96378624; PubMed=8784187;
RA Guddat L.W., Martin J.A., Shan L., Edmundson A.B., Gray W.R.;
RT "Three-dimensional structure of the alpha-conotoxin GI at 1.2-A
RT resolution.";
RL Biochemistry 35:11329-11335(1996).
RN [8]
RP STRUCTURE BY NMR OF GI.
RP MEDLINE=89352562; PubMed=2765514;
RA Kobayashi Y., Ohkubo T., Kyogoku Y., Nishiuchi Y., Sakakibara S.,
RA Braun W., Go N.;
RT "Solution conformation of conotoxin GI determined by 1H nuclear
RT magnetic resonance spectroscopy and distance geometry calculations.";
RL Biochemistry 28:4853-4860(1989).
RN [9]
RP STRUCTURE BY NMR OF GI.
RP MEDLINE=89375269; PubMed=2775719;
RA Pardi A., Galdes A., Florance J., Maniconte D.;
RT "Solution structures of alpha-conotoxin GI determined by two-
RT dimensional NMR spectroscopy.";
RL Biochemistry 28:5494-5501(1989).
RN [10]
RP STRUCTURE BY NMR OF GI.
RP MEDLINE=98321613; PubMed=9660176;
RA Maslennikov I.V., Sobol A.G., Gladky K.V., Lugovskoy A.A.,
RA Ostrovsky A.G., Tsetlin V.I., Ivanov V.T., Arseniev A.S.;

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RT "Two distinct structures of alpha-conotoxin GI in aqueous solution.";

RL Eur. J. Biochem. 254:238-247(1998).

RN [11]

RP STRUCTURE BY NMR OF GI.

RX MEDLINE=98239743; PubMed=9571060;

RA Gehrmann J., Alewood P.F., Craik D.J.;

RT "Structure determination of the three disulfide bond isomers of

RT alpha-conotoxin GI: a model for the role of disulfide bonds in

RT structural stability.";

RL J. Mol. Biol. 278:401-415(1998).

RN [12]

RP STRUCTURE BY NMR OF AN ANTITOXIC ANALOG OF GI.

RX MEDLINE=99438341; PubMed=10508392;

RA Mok K.H., Han K.H.;

RT "NMR solution conformation of an antitoxic analogue of alpha-conotoxin

RT GI: identification of a common nicotinic acetylcholine receptor

RT alpha(1)-subunit binding surface for small ligands and alpha-

RT conotoxins.";

RL Biochemistry 38:11895-11904(1999).

CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they

CC bind to the nicotinic acetylcholine receptors (nAChR) and thus

CC inhibit them. The higher affinity site for alpha-conotoxin GI is

CC the alpha/delta site on mouse muscle-derived BC3H-1 receptor, and

CC the other site (alpha/gamma site) on nicotinic receptors from

CC Torpedo californica electric organ.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type

CC family.

DR PIR; A01782; NTKNAG.

DR PDB; 1N0T; 07-DEC-96.

DR PDB; 1XGA; 16-FEB-99.

DR PDB; 1XGB; 16-FEB-99.

DR PDB; 1XGC; 23-MAR-99.

DR PDB; 1Q53; 06-OCT-99.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;

KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.

FT PEPTIDE 1 15

FT PEPTIDE 1 13

FT DISULFID 2 7

FT DISULFID 3 13

FT MOD_RES 13 13

FT MOD_RES 13 13

FT MOD_RES 15 15

FT MUTAGEN 9 9

FT AMIDATION (G-14 PROVIDE AMIDE GROUP) (IN

FT ALPHA-CONOTOXIN GI).

FT AMIDATION (IN ALPHA-CONOTOXIN GIA).

FT R->A: REDUCTION IN AFFINITY FOR BOTH

FT ALPHA/DELTA AND ALPHA/GAMMA SITES ON

FT BC3H-1 RECEPTORS AND LOSS OF AFFINITY FOR

FT BOTH ALPHA/DELTA AND ALPHA/GAMMA SITES ON

FT TORPEDO RECEPTORS (IN GI).

FT AMIDATION 15 AA; 1628 MW; 2AE73EE50F8C2E19 CRC64;

FT SEQUENCE 15 AA; 1628 MW; 2AE73EE50F8C2E19 CRC64;

Query Match 24.0%; Score 24; DB 1; Length 15;

Best Local Similarity 60.0%; Pred. No. 6.2e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CKPPC 17

DB 3 CNPAC 7

RESULT 5

CXAA2 CONGE STANDARD; PRT; 13 AA.

AC P01520;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-conotoxin GII.

OS Conus geographus (Geography cone).

OS Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=6491;

RN [1]

RP SEQUENCE.

RX MEDLINE=81191854; PubMed=7014556;

RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;

RT "Peptide toxins from Conus geographus venom.";

RL J. Biol. Chem. 256:4734-4740(1981).

RN [2]

RP DISULFIDE BONDS.

RX MEDLINE=84280842; PubMed=6466616;

RA Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,

RA Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,

RA Cruz L.J., Rivier J.;

RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of

RT iodinated derivatives.";

RL Biochemistry 23:2796-2802(1984).

CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they

CC bind to the nicotinic acetylcholine receptors (nAChR) and thus

CC inhibit them.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type

CC family.

DR PIR; A01783; NTKN2G.

DR HSP; F56973; 1B45.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;

KW Acetylcholine receptor inhibitor; Amidation.

FT DISULFID 2 7

FT DISULFID 3 13

FT MOD_RES 13 13

FT MOD_RES 13 13

FT SEQUENCE 13 AA; 1422 MW; DEEB831C39297EBD CRC64;

Query Match 23.0%; Score 23; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. No. 7.9e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CKPPC 17

DB 3 CNPAC 7

RESULT 6

CXAA2 CONST STANDARD; PRT; 13 AA.

ID P28878;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-conotoxin SIA (SIA).

OS Conus striatus (Striated cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=6493;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=91369955; PubMed=1892838;

RA Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,

RA Olivera B.M.;

RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine

RT receptors.";

RL Biochemistry 30:9370-9377(1991).

CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they

CC bind to the nicotinic acetylcholine receptors (nAChR) and thus

CC inhibit them.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type

CC family.

DR PIR; A40312; NTKNAS.

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KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 7
FT DI SULFID 3 13
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457BBD CRC64;
    Query Match 23.0%; Score 23; DB 1; Length 13;
    Best Local Similarity 60.0%; Pred. No. 7.9e+02;
    Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 CKPPC 17
DB 3 CHPAC 7
RESULT 7
ID PSBP PINPS STANDARD; PRT; 13 AA.
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (ORE2) (23 kDa subunit of oxygen
DE evolving system of photosystem II) (Fragment).
GN PSBP.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex (By similarity).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N179) is: 5.9, its MW is: 22 kDa.
CC -!- SIMILARITY: Belongs to the psbp family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;
    Query Match 23.0%; Score 23; DB 1; Length 13;
    Best Local Similarity 40.0%; Pred. No. 7.9e+02;
    Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 6 GKSTNTFCPK 15
DB 3 GEANVFGAP 12
RESULT 8
ID CXAL CONCN STANDARD; PRT; 14 AA.
AC P56973;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin CN1A [Contains: Alpha-conotoxin CN1B].
OS Conus consors (Singed cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101297;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.

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RC TISSUE=Venom;
RX MEDLINE=99255390; PubMed=10320362;
RA Favreau P., Krimm I., le Gall F., Bobenrieth M.J., Lamthanh H.,
RA Bouet P., Servent D., Molgo J., Menez A., Letourneux Y.,
RA Lancelin J.-M.;
RT "Biochemical characterization and nuclear magnetic resonance
RT structure of novel alpha-conotoxins isolated from the venom of Conus
RT consors.";
RL Biochemistry 38:6317-6326(1999).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them. This peptide seems to be a potent and selective
CC blocker of muscular subtype of nAChR.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR; A58963; A58963.
DR PDB; 1B45; 09-JUL-99.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
FT PEPTIDE 1 14
FT PEPTIDE 3 14
FT DISULFID 3 8
FT DISULFID 4 14
FT MOD_RES 14 14
FT HELIX 6 8
FT TURN 9 10
SQ SEQUENCE 14 AA; 1548 MW; DEEE91969BPF5E5BD CRC64;
    Query Match 23.0%; Score 23; DB 1; Length 14;
    Best Local Similarity 60.0%; Pred. No. 8.5e+02;
    Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 CKPPC 17
DB 4 CHPAC 8
RESULT 9
ID CXAL CONCN STANDARD; PRT; 14 AA.
AC P01521;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin MI (MI).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE.
RX MEDLINE=83073458; PubMed=7149738;
RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
RT "Isolation and structure of a peptide toxin from the marine snail
RT Conus magus.";
RL Arch. Biochem. Biophys. 218:329-334(1982).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=84032400; PubMed=6630187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RT "Conotoxin MI. Disulfide bonding and conformational states.";
RL J. Biol. Chem. 258:12247-12251(1983).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR; A01784; NTKN1M.

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DR HSP; P56973; 1B45.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 FT Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 3 8
 FT DISULFID 4 14
 FT MOD RES 14 14
 SQ SEQUENCE 14 AA; 1499 MW; DEEE1898BF5E5BD CRC64;
 Query Match 23.0%; Score 23; DB 1; Length 14;
 Best Local Similarity 60.0%; Pred. No. 8.5e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 13 CKPPC 17
 Db 4 CHPAC 8
 RESULT 10
 CX1B CONBE STANDARD; PRT; 15 AA.
 AC P56624;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Conotoxin BetXib.
 OS Conus betulinus (Beech cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89764;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20058566; PubMed=10591037;
 RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
 RT "Studies on conotoxins of Conus betulinus.";
 RL J. Nat. Toxins 8:341-349(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1642.5; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
 KW Neurotoxin; Toxin.
 FT DISULFID 1 9
 FT DISULFID 2 12
 FT DISULFID 6 13
 SQ SEQUENCE 15 AA; 1650 MW; 3749B4F08E311337 CRC64;
 Query Match 23.0%; Score 23; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 9.1e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 13 CKPPC 17
 Db 2 CELPC 6
 RESULT 11
 CXA2 CONAL STANDARD; PRT; 15 AA.
 AC P56640;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-conotoxin AuiB.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99003392; PubMed=9786965;
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RT "Alpha-conotoxin AuiB selectively blocks alpha3 beta4 nicotinic
 acetylcholine receptors and nicotine-evoked norepinephrine release.";
 RL J. Neurosci. 18:8571-8579(1998).
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they

RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RA Olivera B.M., McIntosh J.M.;
 RT "Alpha-conotoxin AuiB selectively blocks alpha3 beta4 nicotinic
 acetylcholine receptors and nicotine-evoked norepinephrine release.";
 RL J. Neurosci. 18:8571-8579(1998).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=20187585; PubMed=10722709;
 RA Cho J.H., Mok K.H., Olivera B.M., McIntosh J.M., Park K.H., Han K.H.;
 RT "Nuclear magnetic resonance solution conformation of alpha-conotoxin
 AuiB, an alpha(3)beta(4) subtype-selective neuronal nicotinic
 acetylcholine receptor antagonist.";
 RL J. Biol. Chem. 275:8680-8685(2000).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=22359066; PubMed=12376538;
 RA Dutton J.L., Bansal P.S., Hogg R.C., Adams D.J., Alewood P.F.,
 RA Craik D.J.;
 RT "A new level of conotoxin diversity, a non-native disulfide bond
 connectivity in alpha-conotoxin AuiB reduces structural definition
 but increases biological activity.";
 RL J. Biol. Chem. 277:48849-48857(2002).
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 bind to the nicotinic acetylcholine receptors (nAChR) and thus
 inhibit them. This peptide blocks mammalian nicotinic
 acetylcholine receptors composed of alpha-3/beta-4 subunits.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 family.
 DR PDB; 1DG2; 23-MAY-00.
 DR PDB; 1MXN; 30-DEC-02.
 DR PDB; 1NXP; 30-DEC-02.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 FT DISULFID 2 8
 FT DISULFID 3 15
 FT MOD RES 15 15
 SQ SEQUENCE 15 AA; 1578 MW; 84EFE95FDC700155 CRC64;
 Query Match 23.0%; Score 23; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 PPC 17
 Db 6 PPC 8
 RESULT 12
 CXA1 CONAL STANDARD; PRT; 16 AA.
 AC P56639;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-conotoxin AuiA.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99003392; PubMed=9786965;
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RT "Alpha-conotoxin AuiB selectively blocks alpha3 beta4 nicotinic
 acetylcholine receptors and nicotine-evoked norepinephrine release.";
 RL J. Neurosci. 18:8571-8579(1998).
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they

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CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them. This peptide blocks mammalian nicotinic
 CC acetylcholine receptors composed of alpha-3/beta-4 subunits.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 CC family.
 DR PIR; A59045; A59045.
 DR HSSP; P50984; 1PEN.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT MOD_RES 3 16
 FT SEQUENCE 16 AA; 1731 MW; 1E310FB8FDC7001 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;
 QY 15 PPC 17
 DB 6 PPC 8

RESULT 13
 CXA3_CONAL STANDARD; PRT; 16 AA.
 AC P56641;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin AUC.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99003392; PubMed=9786965;
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RA Olivera B.M., McIntosh J.M.;
 RT "Alpha-conotoxin AUC selectively blocks alpha3 beta4 nicotinic
 RT acetylcholine receptors and nicotine-evoked norepinephrine release."
 RL J. Neurosci. 18:8571-8579(1998).
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them. This peptide blocks mammalian nicotinic
 CC acetylcholine receptors composed of alpha-3/beta-4 subunits.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1667.6; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 CC family.
 DR PIR; C59045; C59045.
 DR HSSP; P50984; 1PEN.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 16 16
 FT SEQUENCE 16 AA; 1673 MW; 1E310D3B8FDC7001 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;
 QY 15 PPC 17
 DB 6 PPC 8

RESULT 14

CXAA_CONPE STANDARD; PRT; 16 AA.
 AC P50984;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin PnIA.
 OS Conus pennaceus (Feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=37335;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=94347719; PubMed=8068627;
 RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
 RA Fainzilber M., Zlotkin E.;
 RA Spira M.E., Zlotkin E.;
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 RT acetylcholine receptors."
 RT Biochemistry 33:9523-9529(1994).
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [2]
 RP SULFATION OF TYR-15.
 RX MEDLINE=99242956; PubMed=10226369;
 RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
 RA Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
 RT phosphopeptides by electrospray, matrix-assisted laser
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 RT spectrometry."
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [3]

RN X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE=96311277; PubMed=8740364;
 RA Hu S.-H., Gehrman J., Guddat L.W., Alewood P.F., Craik D.J.,
 RA Martin J.L.;
 RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
 RT antagonist, alpha-conotoxin PnIA from Conus pennaceus."
 RL Structure 4:417-423(1996).
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them. In contrast to other alpha-conotoxins, which are
 CC selective for vertebrate skeletal muscle nAChR, the Conus
 CC pennaceus alpha-conotoxins block nAChR in mollusks.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 CC family.
 DR PIR; A54877; A54877.
 DR PDB; 1PEN; 21-APR-97.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16
 FT MOD_RES 2 4
 FT HELIX 6 11
 FT TURN 13 16
 FT SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;
 QY 15 PPC 17
 DB 6 PPC 8

Job time : 15 secs

RESULT 15

CXAB CONPE
 ID CXAB CONPE STANDARD; PRT; 16 AA.
 AC P50985;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin PnIB.
 OS Conus pennaceus (Feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=37335;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=94347719; PubMed=8068627;
 RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
 RA Spira M.E., Zlotkin E.;
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 RT acetylcholine receptors.";
 RL Biochemistry 33:9523-9529(1994).
 RN [2]
 RP SULFATION OF TYR-15.
 RX MEDLINE=99242956; PubMed=10226369;
 RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
 RA Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
 RT phosphopeptides by electrospray, matrix-assisted laser
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 RT spectrometry.";
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE=97444322; PubMed=9298951;
 RA Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
 RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
 RT comparison with alpha-conotoxins PnIA and GI.";
 RL Biochemistry 36:11323-11330(1997).
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them. In contrast to other alpha-conotoxins, which are
 CC selective for vertebrate skeletal muscle nAChR, the Conus
 CC pennaceus alpha-conotoxins block nAChR in mollusks.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 CC family.
 DR PIR; B54877.
 DR PDB; 1AKG; 20-MAY-98.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15 SULFATION.
 FT MOD_RES 16 16 AMIDATION.
 FT HELIX 2 4
 FT HELIX 6 11
 FT TURN 13 16
 SQ SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;

Query Match

23.0%; Score 23; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.7e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PPC 17

Db 6 PPC 8

Search completed: September 5, 2004, 10:54:59

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:51:46 ; Search time 57 Seconds
(without alignments)
94.102 Million cell updates/sec

Title: US-09-761-636a-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCCKPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5061

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	27.0	13	13	O8QZ5 fugu rubrip
2	26	26.0	13	12	Q918T4 human papil
3	26	26.0	13	12	Q918T6 human papil
4	26	26.0	16	12	Q918U2 human papil
5	26	26.0	16	12	Q918T1 human papil
6	26	26.0	16	12	Q918U8 human papil
7	26	26.0	16	12	Q918U6 human papil
8	26	26.0	16	12	Q918U4 human papil
9	26	26.0	16	12	Q918T9 human papil
10	26	26.0	17	3	Q9C0S9
11	26	26.0	17	3	Q9C0S6
12	26	26.0	17	3	Q8NIJ7
13	26	26.0	17	3	Q8NIJ6
14	26	26.0	17	3	Q9C0S7
15	26	26.0	17	3	Q9C0S8
16	26	26.0	17	3	Q9C1Q8

17	26	26.0	17	3	Q8J168
18	26	26.0	17	3	Q870J0
19	26	26.0	17	3	Q96TQ4
20	26	26.0	17	3	Q94758
21	26	26.0	17	3	Q72885
22	26	26.0	17	3	Q727U6
23	26	26.0	17	3	Q727U5
24	25	25.0	12	5	Q8MY01
25	25	25.0	17	2	Q55091
26	24	24.0	13	11	O54809
27	24	24.0	16	11	Q9ERP8
28	24	24.0	17	2	Q9P581
29	23	23.0	12	13	Q9P867
30	23	23.0	14	4	Q16332
31	23	23.0	16	5	Q9TWS1
32	23	23.0	16	6	O77491
33	22	22.0	11	7	O77872
34	22	22.0	11	7	O77873
35	22	22.0	11	7	O77871
36	22	22.0	14	2	Q9R5Q9
37	22	22.0	14	4	Q16484
38	22	22.0	16	12	Q84055
39	21.5	21.5	15	13	Q8AX09
40	21	21.0	12	12	Q85666
41	21	21.0	13	6	Q9GUJ2
42	21	21.0	13	11	Q9QV13
43	21	21.0	13	13	P82821
44	21	21.0	13	13	P82822
45	21	21.0	14	2	Q43905

ALIGNMENTS

RESULT 1

O8QZ5	PRELIMINARY;	PRT;	13 AA.
AC O8QZ5			
DT 01-JUN-2002 (Tremblrel. 21, Created)			
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)			
DE Guanine nucleotide binding protein (Fragment).			
GN GNAO.			
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;			
OC Tetraodontidae; Tetraodontidae; Takifugu.			
OX NCBI_TaxID=31033;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=97129408; PubMed=8973916;			
RA Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;			
RT "G protein alpha subunit multigene family in the Japanese puffer fish			
Fugu rubripes: PCR from a compact vertebrate genome.";			
RL Genome Res. 6:1207-1215 (1996).			
DR EMBL; L79891; AAL77640.1; -.			
DR GO; GO:0004871; F:signal transducer activity; IEA.			
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.			
DR InterPro; IPR001019; Gprotein_alpha.			
DR Pfam; PF00503; G-alpha; 1.			
FT NON_TER 1 1			
FT NON_TER 13 13			
SQ SEQUENCE 13 AA; 1336 MW; 465B59640B44B5B3 CRC64;			

Query Match 27.0%; Score 27; DB 13; Length 13;

Best Local Similarity 75.0%; Pred. No. 7e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGKST 9

Db 1 AGESGKST 8

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RESULT 2
Q918T4 ID Q918T4 PRELIMINARY; PRT; 13 AA.
AC Q918T4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC7;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407220; AAL01406.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 26.0%; Score 26; DB 12; Length 13;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
Db 4 CVS--GQNTNT 12

RESULT 3
Q918T6 ID Q918T6 PRELIMINARY; PRT; 13 AA.
AC Q918T6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC6;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407219; AAL01403.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 26.0%; Score 26; DB 12; Length 13;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
Db 4 CVS--GQNTNT 12

RESULT 4
Q918U2 ID Q918U2 PRELIMINARY; PRT; 16 AA.
AC Q918U2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

RESULT 5
Q918T1 ID Q918T1 PRELIMINARY; PRT; 16 AA.
AC Q918T1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC8;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407221; AAL01409.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match 26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
Db 7 CVS--GQNTNT 15

RESULT 6
Q918U8 ID Q918U8 PRELIMINARY; PRT; 16 AA.
AC Q918U8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;


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RN  SEQUENCE FROM N.A.
RP  STRAIN=HPV16E2CC1;
RA  Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human Papillomavirus type 16
RL  cervical cancer isolates from Australia and New Caledonia.";
DR  EMBL; AF407214; AAL01388.1; -.
FT  NON_TER 1
SQ  SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match      26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY  1 CASELGKSTNT 11
Db  | | | | |
    7 CVS--GQNTNT 15

RESULT 7
ID  Q918U6 PRELIMINARY; PRT; 16 AA.
AC  Q918U6;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  E1 protein (Fragment).
GN  E1.
OS  Human papillomavirus type 16.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Papillomavirus.
OX  NCBI_TaxID=10581;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=HPV16E2CC2;
RA  Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human Papillomavirus type 16
RL  cervical cancer isolates from Australia and New Caledonia.";
DR  EMBL; AF407215; AAL01391.1; -.
FT  NON_TER 1
SQ  SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match      26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY  1 CASELGKSTNT 11
Db  | | | | |
    7 CVS--GQNTNT 15

RESULT 8
ID  Q918U4 PRELIMINARY; PRT; 16 AA.
AC  Q918U4;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  E1 protein (Fragment).
GN  E1.
OS  Human papillomavirus type 16.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Papillomavirus.
OX  NCBI_TaxID=10581;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=HPV16E2CC3;
RA  Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human Papillomavirus type 16
RL  cervical cancer isolates from Australia and New Caledonia.";
DR  EMBL; AF407216; AAL01394.1; -.
FT  NON_TER 1
SQ  SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match      26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY  1 CASELGKSTNT 11
Db  | | | | |
    7 CVS--GQNTNT 15

RESULT 9
ID  Q918T9 PRELIMINARY; PRT; 16 AA.
AC  Q918T9;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  E1 protein (Fragment).
GN  E1.
OS  Human papillomavirus type 16.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Papillomavirus.
OX  NCBI_TaxID=10581;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=HPV16E2CC5;
RA  Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human Papillomavirus type 16
RL  cervical cancer isolates from Australia and New Caledonia.";
DR  EMBL; AF407218; AAL01400.1; -.
FT  NON_TER 1
SQ  SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match      26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY  1 CASELGKSTNT 11
Db  | | | | |
    7 CVS--GQNTNT 15

RESULT 10
ID  Q9C0S9 PRELIMINARY; PRT; 17 AA.
AC  Q9C0S9;
DT  01-JUN-2001 (TREMBLrel. 17, Created)
DT  01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT  01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE  E1-alpha (Fragment).
GN  TEF1.
OS  Claviceps purpurea (Ergot fungus).
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC  Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
OX  NCBI_TaxID=5111;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Clp-1, and Clp-2;
RA  Toolley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
RA  Kuldau G.A.;
RT  "Characterization of Claviceps species pathogenic on sorghum by
RL  sequence analysis of the beta-tubulin gene intron 3 region and E1-
RL  alpha gene intron 4.";
DR  Mycologia 93:541-551(2001).
DR  EMBL; AF255889; AAK37634.1; -.
DR  EMBL; AF255890; AAK37635.1; -.
FT  NON_TER 1
SQ  SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;
```

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Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9
   |:||||:
Db 8 AELGKGS 15

RESULT 11
Q9C0S6 PRELIMINARY; PRT; 17 AA.
AC Q9C0S6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EFl-alpha (Fragment).
GN TEFL.
OS Claviceps africana.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
OX NCBI_TaxID=83212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cla-2, Cla-7, Cla-1, and Cla-2;
RA Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
RA Kulda G.A.;
RT "Characterization of Claviceps species pathogenic on sorghum by
RT sequence analysis of the beta-tubulin gene intron 3 region and EFl-
RT alpha gene intron 4."
RL Mycologia 93:541-551(2001).
DR EMBL; AF255896; AAK37641.1; -
DR EMBL; AF255897; AAK37642.1; -
DR EMBL; AF255898; AAK37643.1; -
DR EMBL; AF255899; AAK37644.1; -
DR NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9
   |:||||:
Db 8 AELGKGS 15

RESULT 12
Q8NIJ7 PRELIMINARY; PRT; 17 AA.
AC Q8NIJ7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Translation elongation factor 1 alpha (fragment).
OS Fusarium solani.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=169388;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T-8, 3-bean, and 71-tomato;
RA Li S.;
RT "Molecular characterization of Fusarium solani isolates based on the
RT translation elongation factor 1 alpha gene."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY043480; AAK95394.1; -
DR EMBL; AY043481; AAK95395.1; -
DR EMBL; AY043482; AAK95396.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.

Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9
   |:||||:
Db 8 AELGKGS 15

RESULT 13
Q8NIJ6 PRELIMINARY; PRT; 17 AA.
ID Q8NIJ6;
AC Q8NIJ6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Translation elongation factor 1-alpha (fragment).
OS Fusarium solani f. sp. glycines.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=108887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Various strains;
RA Li S.;
RT "Molecular characterization of Fusarium solani f. sp. glycines based
RT on the translation elongation factor 1-alpha gene."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF395645; AAM73735.1; -
DR EMBL; AF395646; AAM73736.1; -
DR EMBL; AF395647; AAM73737.1; -
DR EMBL; AF395648; AAM73738.1; -
DR EMBL; AF395649; AAM73739.1; -
DR EMBL; AF395650; AAM73740.1; -
DR EMBL; AF395651; AAM73741.1; -
DR EMBL; AF395652; AAM73742.1; -
DR EMBL; AF395653; AAM73743.1; -
DR EMBL; AF395654; AAM73744.1; -
DR EMBL; AF395655; AAM73745.1; -
DR EMBL; AF395656; AAM73746.1; -
DR EMBL; AF395657; AAM73747.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9
   |:||||:
Db 8 AELGKGS 15

RESULT 14
Q9C0S7 PRELIMINARY; PRT; 17 AA.
ID Q9C0S7;
AC Q9C0S7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EFl-alpha (fragment).
GN TEFL.
OS Claviceps sorghicola.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
OX NCBI_TaxID=83213;

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FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9
   |:||||:
Db 8 AELGKGS 15

RESULT 13
Q8NIJ6 PRELIMINARY; PRT; 17 AA.
ID Q8NIJ6;
AC Q8NIJ6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Translation elongation factor 1-alpha (fragment).
OS Fusarium solani f. sp. glycines.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=108887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Various strains;
RA Li S.;
RT "Molecular characterization of Fusarium solani f. sp. glycines based
RT on the translation elongation factor 1-alpha gene."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF395645; AAM73735.1; -
DR EMBL; AF395646; AAM73736.1; -
DR EMBL; AF395647; AAM73737.1; -
DR EMBL; AF395648; AAM73738.1; -
DR EMBL; AF395649; AAM73739.1; -
DR EMBL; AF395650; AAM73740.1; -
DR EMBL; AF395651; AAM73741.1; -
DR EMBL; AF395652; AAM73742.1; -
DR EMBL; AF395653; AAM73743.1; -
DR EMBL; AF395654; AAM73744.1; -
DR EMBL; AF395655; AAM73745.1; -
DR EMBL; AF395656; AAM73746.1; -
DR EMBL; AF395657; AAM73747.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9
   |:||||:
Db 8 AELGKGS 15

RESULT 14
Q9C0S7 PRELIMINARY; PRT; 17 AA.
ID Q9C0S7;
AC Q9C0S7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EFl-alpha (fragment).
GN TEFL.
OS Claviceps sorghicola.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
OX NCBI_TaxID=83213;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cjap-2, and Cjap-4;
RA Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
RA Kuldau G.A.;
RT "Characterization of Claviceps species pathogenic on sorghum by
RT sequence analysis of the beta-tubulin gene intron 3 region and EF1-
RT alpha gene intron 4."
RL Mycologia 93:541-551(2001).
DR EMBL; AF255894; AAK37639.1; -.
DR EMBL; AF255895; AAK37640.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 8 AAELGKGS 15

RESULT 15
Q9C0S8 PRELIMINARY; PRT; 17 AA.
AC Q9C0S8;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE EF1-alpha (Fragment).
GN TEF1.
OS Claviceps paspali (paspalum straggers ergot).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
OX NCBI_TaxID=40601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cpas-1, and Cpas-2;
RA Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
RA Kuldau G.A.;
RT "Characterization of Claviceps species pathogenic on sorghum by
RT sequence analysis of the beta-tubulin gene intron 3 region and EF1-
RT alpha gene intron 4."
RL Mycologia 93:541-551(2001).
DR EMBL; AF255892; AAK37637.1; -.
DR EMBL; AF255893; AAK37638.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 8 AAELGKGS 15

```

Search completed: September 5, 2004, 10:56:03
Job time : 58 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:48:30 ; Search time 62 seconds
(without alignments)
77.473 Million cell updates/sec

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTRFCRPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 470470

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	17	AAU04527	AAU04527 VEGF base
2	97	97.0	17	AAU04550	AAU04550 VEGF base
3	97	97.0	17	AAU04546	AAU04546 VEGF base
4	93	93.0	17	AAU04547	AAU04547 VEGF base
5	93	93.0	17	AAU04551	AAU04551 VEGF base
6	93	93.0	17	AAU04549	AAU04549 VEGF base
7	89	89.0	17	AAU04548	AAU04548 VEGF base
8	72	72.0	13	AAU04524	AAU04524 VEGF base
9	69	69.0	13	AAU04534	AAU04534 VEGF base
10	65	65.0	13	AAU04535	AAU04535 VEGF base
11	65	65.0	13	AAU04537	AAU04537 VEGF base
12	61	61.0	13	AAU04536	AAU04536 VEGF base
13	48	48.0	14	AAU04542	AAU04542 VEGF base
14	39	39.0	8	AAU08482	AAU08482 Peptide #
15	37	37.0	10	AAU10122	AAU10122 Peptide #
16	37	37.0	12	AAU57039	AAU57039 Peptide #
17	35	35.0	17	AAU57039	AAU57039 Peptide #
18	33	33.0	16	AAU57039	AAU57039 Peptide #
19	32	32.0	9	AAU57039	AAU57039 Peptide #
20	32	32.0	11	AAU57039	AAU57039 Peptide #
21	32	32.0	12	AAU57039	AAU57039 Peptide #
22	32	32.0	12	AAU57039	AAU57039 Peptide #
23	32	32.0	12	AAU57039	AAU57039 Peptide #
24	32	32.0	12	AAU57039	AAU57039 Peptide #
25	32	32.0	12	AAU57039	AAU57039 Peptide #

26	32	32.0	12	4	AAU46653	AAU46653 HIV-1 Tat
27	32	32.0	13	4	AAU46654	AAU46654 HIV-1 Tat
28	32	32.0	13	4	AAU08459	AAU08459 Peptide C
29	32	32.0	13	5	ABJ04094	ABJ04094 Immunoglob
30	32	32.0	14	3	AAU66872	AAU66872 T cell an
31	32	32.0	14	4	AAU46655	AAU46655 HIV-1 Tat
32	32	32.0	15	4	AAU46656	AAU46656 HIV-1 Tat
33	32	32.0	15	4	ABP24824	ABP24824 HIV DR su
34	32	32.0	15	6	ABR81834	ABR81834 HIV Tat T
35	32	32.0	16	2	AAU25715	AAU25715 CB1 parti
36	32	32.0	16	2	AAU57342	AAU57342 Peptide f
37	32	32.0	16	2	AAU14288	AAU14288 Citrus dl
38	32	32.0	16	3	AAU66903	AAU66903 T cell an
39	32	32.0	16	3	AAU66503	AAU66503 HIV-1 Tat
40	32	32.0	16	5	ABR88471	ABR88471 C aulicus
41	32	32.0	16	6	ABR81821	ABR81821 HIV Tat r
42	32	32.0	17	3	AAU25943	AAU25943 Pl mimoto
43	32	32.0	17	3	AAU26024	AAU26024 Human IGE
44	32	32.0	17	4	AAU46658	AAU46658 HIV-1 Tat
45	32	32.0	17	4	AAU16668	AAU16668 Peptide #

ALIGNMENTS

RESULT 1

AAU04527
ID AAU04527 standard; protein; 17 AA.

XX AC AAU04527;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based bicyclic dimeric peptide #1.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

XX KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

XX KW diabetes induced neovascular sequelae; rheumatoid arthritis;

XX KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key

XX FT Disulfide-bond 1..13

XX FT Disulfide-bond /note= "This bond cyclises the peptide"

XX FT Disulfide-bond 17

XX FT /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide, or to residue 1 of the sequence appearing as AAU04528, also forming a dimeric peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

XX Claim 59; Page 32; 102pp; English.

CC The sequence represents a dimeric bicyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a
CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation, diabetes induced neovascular
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere
CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 100; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e-08; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 CASELGKSTNTFCCKPC 17
Db 1 CASELGKSTNTFCCKPC 17
|||||

RESULT 2
AAU04550
ID AAU04550 standard; peptide; 17 AA.

XX AC AAU04550;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based bicyclic dimeric peptide #7.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX KW diabetes induced neovascular sequelae; rheumatoid arthritis;
XX KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"

FT Disulfide-bond 17

FT /note= "A disulfide bond forms between residue 17 and
FT residue 1 of the sequence appearing as AAU04528, forming
FT a dimeric peptide"

XX PN WC200152875-A1.

XX PD 26-JUL-2001.

XX XX 18-JAN-2001; 2001WO-US001533.

XX XX 18-JAN-2000; 2000US-0176293P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.

XX Example 26; Page 49; 102pp; English.

PS The sequence represents a dimeric bicyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a
CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation, diabetes induced neovascular
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere
CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy
XX
SQ Sequence 17 AA;

Query Match 97.0%; Score 97; DB 4; Length 17;

Best Local Similarity 94.1%; Pred. No. 1.7e-07;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCCKPC 17

Db 1 CASELGKSTNTFCCKPC 17
|||||

RESULT 3

AAU04546

ID AAU04546 standard; peptide; 17 AA.

XX AC AAU04546;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based bicyclic dimeric peptide #3.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX KW diabetes induced neovascular sequelae; rheumatoid arthritis;
XX KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"

FT Disulfide-bond 17

OY 1 CASELGKSTNTFCRPPC 17
 DB 1 CASELGKSTNTFCRPPC 17

RESULT 5
 AAU04551
 ID AAU04551 standard; peptide; 17 AA.
 XX AAU04551;
 AC AAU04551;
 XX AAU04551;
 DT 26-SEP-2001 (first entry)
 XX VEGF based bicyclic dimeric peptide #8.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX Synthetic.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..13
 FT /note= "This bond cyclises the peptide"
 FT Disulfide-bond 17
 FT /note= "A disulfide bond forms between residue 17 and
 FT residue 1 of the sequence appearing as AAU04528, forming
 FT a dimeric peptide"
 XX WO200152875-A1.
 XX 26-JUL-2001.
 XX 18-JAN-2001; 2001WO-US001533.
 XX 18-JAN-2000; 2000US-0176293P.
 XX 16-MAY-2000; 2000US-0204590P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX Example 26; Page 49; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX Sequence 17 AA;
 SQ

Query Match 93.0%; Score 93; DB 4; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.9e-07;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CASELGKSTNTFCRPPC 17
 DB 1 CASELGKSTNTFCRPPC 17

RESULT 6
 AAU04549
 ID AAU04549 standard; peptide; 17 AA.
 XX AAU04549;
 AC AAU04549;
 XX 26-SEP-2001 (first entry)
 XX VEGF based bicyclic dimeric peptide #6.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX Synthetic.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..13
 FT /note= "This bond cyclises the peptide"
 FT Disulfide-bond 17
 FT /note= "A disulfide bond forms between residue 17 and
 FT residue 17 of an identical peptide to form a dimeric
 FT peptide"
 XX WO200152875-A1.
 XX 26-JUL-2001.
 XX 18-JAN-2001; 2001WO-US001533.
 XX 18-JAN-2000; 2000US-0176293P.
 XX 16-MAY-2000; 2000US-0204590P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX Example 26; Page 49; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 17 AA;

Query Match 93.0%; Score 93; DB 4; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.9e-07;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCPPC 17
 |||||:||||:|||||
 Db 1 CASELGRSTNSFCPPC 17

RESULT 7
 AAU04548
 ID AAU04548 standard; peptide; 17 AA.
 AC
 XX AAU04548;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based bicyclic dimeric peptide #5.

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT Disulfide-bond 1..13
 FT /note= "This bond cyclises the peptide"
 FT Disulfide-bond 17
 FT /note= "A disulfide bond forms between residue 17 and
 FT residue 17 of an identical peptide to form a dimeric
 FT peptide"

XX W0200152875-A1.
 XX
 XX 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 XX 16-MAY-2000; 2000US-0204590P.
 XX (LUDW-) LUDWIG INST CANCER RES.

PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment

PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

XX Example 26; Page 49; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX

SQ Sequence 17 AA;

Query Match 89.0%; Score 89; DB 4; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.7e-06;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCPPC 17
 |||||:||||:|||||
 Db 1 CASDVGKSTNTWCKPPC 17

RESULT 8
 AAU04524
 ID AAU04524 standard; peptide; 13 AA.
 AC AAU04524;
 XX

DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 1.

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT Disulfide-bond 1..13
 FT /note= "This bond cyclises the peptide"

XX W0200152875-A1.
 XX
 XX 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 XX 16-MAY-2000; 2000US-0204590P.

XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX XX WPI; 2001-442248/47.
 XX DR
 XX XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 XX PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 XX PT residues.
 XX XX
 XX PS Claim 49; Page 32; 102pp; English.
 XX XX
 XX CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC CC whose 3-dimensional structure is modelled on the expose loop of human
 CC CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC CC beta carbon separation distances on opposite antiparallel strands of a
 CC CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC CC to cyclisation are used to interfere with angiogenesis,
 CC CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC CC trauma, substance-induced neovascularisation of the liver, excessive
 CC CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC CC infection. The peptides are also used to modulate vascular permeability
 CC CC in a mammal (the mammal has a condition characterised by fluid
 CC CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC CC or brain. The peptides are used to image blood vessels and lymphatic
 CC CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC CC are also used in combination with an anti-inflammatory agent, to treat a
 CC CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC CC diabetic retinopathy
 XX XX
 XX SQ Sequence 13 AA;
 Query Match 72.0%; Score 72; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00073;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CASELGKSTNTFC 13
 Db 1 CASELGKSTNTFC 13
 RESULT 9
 AAU04534
 ID AAU04534 standard; peptide; 13 AA.
 XX AC AAU04534;
 XX XX
 XX DT 26-SEP-2001 (first entry)
 XX DE VEGF based monocyclic peptide 12.
 XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW KW diabetic retinopathy; chronic inflammation; cyclic.
 XX OS Synthetic.
 XX FH Key
 XX FT Disulfide-bond 1..13
 XX FT /note= "This bond cyclises the peptide"

XX PN WO200152875-A1.
 XX PD 26-JUL-2001.
 XX PF 18-JAN-2001; 2001WO-US0001533.
 XX PR 18-JAN-2000; 2000US-0176293P.
 XX PR 16-MAY-2000; 2000US-0204590P.
 XX XX (LUDW-) LUDWIG INST CANCER RES.
 XX XX Achen MG, Hughes RA, Stacker S, Cendron A;
 XX XX WPI; 2001-442248/47.
 XX XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 XX PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 XX PT residues.
 XX XX
 XX PS Example 25; Page 47; 102pp; English.
 XX XX
 XX CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC CC whose 3-dimensional structure is modelled on the expose loop of human
 CC CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC CC beta carbon separation distances on opposite antiparallel strands of a
 CC CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC CC to cyclisation are used to interfere with angiogenesis,
 CC CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC CC trauma, substance-induced neovascularisation of the liver, excessive
 CC CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC CC infection. The peptides are also used to modulate vascular permeability
 CC CC in a mammal (the mammal has a condition characterised by fluid
 CC CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC CC or brain. The peptides are used to image blood vessels and lymphatic
 CC CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC CC are also used in combination with an anti-inflammatory agent, to treat a
 CC CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC CC diabetic retinopathy
 XX XX
 XX SQ Sequence 13 AA;
 Query Match 69.0%; Score 69; DB 4; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.002;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CASELGKSTNTFC 13
 Db 1 CASELGKSTNTFC 13
 RESULT 10
 AAU04535
 ID AAU04535 standard; peptide; 13 AA.
 XX AC AAU04535;
 XX XX
 XX DT 26-SEP-2001 (first entry)
 XX DE VEGF based monocyclic peptide 13.
 XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 XX Disulfide-bond 1. 13
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

PS Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascular sequelae, or chronic liver
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascularisation of the liver, excessive
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX Sequence 13 AA;

Query Match 65.0%; Score 65; DB 4; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.008;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTWTF 13

|||||:||||

Db 1 CASELGKTSNTFC 13

RESULT 11

AAU04537

AAU04537 standard; peptide; 13 AA.
 AAU04537;
 XX
 XX 26-SRP-2001 (first entry)
 XX VEGF based monocyclic peptide 15.
 DE
 DE
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 XX Disulfide-bond 1. 13
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

PS Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX Sequence 13 AA;

Query Match 65.0%; Score 65; DB 4; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.008;


```

XX SQ Sequence 14 AA;
Query Match 48.0%; Score 48; DB 4; Length 14;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TNTFCPPC 17
Db 1 TNTFCPPC 9

RESULT 14
AAU08481
ID AAU08481 standard; peptide; 8 AA.
XX
AC AAU08481;
XX
DT 21-NOV-2001 (first entry)
XX
DE Peptide #3 inhibiting human VEGF-C mediated activation of VEGFR-3.
XX
KW Human; vascular endothelial growth factor; VEGF-C; vasculogenesis;
KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;
KW VEGFR-3.
XX
OS Homo sapiens.
XX
PN WO200162942-A2.
XX
PD 30-AUG-2001.
XX
PF 26-FEB-2001; 2001WO-US006113.
XX
PR 25-FEB-2000; 2000US-0185205P.
PR 18-MAY-2000; 2000US-0205331P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA OY.
XX
PI Alitalo K, Jeltsch MM;
XX
WPI; 2001-536640/59.
XX
PT Polypeptides that bind cellular receptors for vascular endothelial growth
PT factors, polynucleotides encoding them.
XX
PS Claim 64; Page 147; 261pp; English.
XX
CC The present invention relates to polypeptides that bind cellular
CC receptors for vascular endothelial growth factors (VEGFs), the
CC polynucleotides encoding them, and their use for identifying agents that
CC modulate interactions between VEGFs and their receptors. VEGFs and their
CC receptors play an important role in vasculogenesis, the development of
CC the embryonic vasculature from early differentiating endothelial cells
CC and angiogenesis, the process of forming new blood vessels from pre-
CC existing ones. Modulators of interactions between VEGF and its receptors
CC may be used to treat dysfunction of the endothelial cell regulatory
CC system. Such disorders include cancers, abnormal angiogenesis,
CC proliferative retinopathies, age-related macular degeneration, rheumatoid
CC arthritis and psoriasis. The polypeptides of the invention exhibit unique
CC receptor binding profiles compared to known naturally occurring VEGFs.
CC AAU08479-AAU08483 represents peptides which inhibit human VEGF-C mediated
CC activation of VEGFR-3
XX
SQ Sequence 8 AA;
Query Match 39.0%; Score 39; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TNTFCPPC 16

```

```

Db 1 TNTFCPP 8
|||||
RESULT 15
AAW10122
ID AAW10122 standard; protein; 10 AA.
XX
AC AAW10122;
XX
DT 18-SEP-1997 (first entry)
XX
DE Human agouti signalling protein fragment #10.
XX
KW Agouti signalling protein; ASP; depigmenting activity; cosmetic;
KW hyperpigmentary condition; melasma photoageing spots; solar keratosis;
KW post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
KW vitiligo; leucoderma; albinism; hair greying.
XX
OS Homo sapiens.
XX
PN WO9700892-A2.
XX
PD 09-JAN-1997.
XX
PF 21-JUN-1996; 96WO-US010695.
PR 23-JUN-1995; 95US-0000436P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Hearing VJ;
XX
WPI; 1997-087323/08.
XX
PT New agouti signal protein, peptide(s) and nucleic acids - used for
PT altering melanin prodn., for treating e.g. melasma photo-ageing spots,
PT solar keratosis or vitiligo.
XX
PS Claim 26; Page 12; 67pp; English.
XX
CC The sequences given in AAW10101-29 are biologically active peptides and
CC fragments of the agouti signalling protein (ASP) which have depigmenting
CC activity. These peptides are useful for cosmetic purposes and for
CC clinical application in the prevention or treatment of various
CC hyperpigmentary conditions and diseases such as melasma photoageing
CC spots, solar keratosis, and post-inflammatory hyperpigmentation such as
CC occurs at sites of wound healing. They can also be used to provide
CC enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some
CC forms of albinism and hair greying
XX
SQ Sequence 10 AA;
Query Match 37.0%; Score 37; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 95;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 STNTFCPP 16
Db 1 ATNDSCKPP 9
|||||
Search completed: September 5, 2004, 10:54:38
Job time : 63 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:56:07 ; Search time 66 Seconds
(without alignments)
81.153 Million cell updates/sec

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 230634

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	97	97.0	17	9	US-09-761-636A-27
3	97	97.0	17	9	US-09-761-636A-31
4	93	93.0	17	9	US-09-761-636A-28
5	93	93.0	17	9	US-09-761-636A-30
6	93	93.0	17	9	US-09-761-636A-32
7	89	89.0	17	9	US-09-761-636A-29
8	72	72.0	13	9	US-09-761-636A-5
9	69	69.0	13	9	US-09-761-636A-15
10	65	65.0	13	9	US-09-761-636A-16
11	65	65.0	13	9	US-09-761-636A-17
12	61	61.0	13	9	US-09-761-636A-18
13	37	37.0	10	12	US-10-435-238-22
14	32	32.0	7	9	US-09-805-761-61
15	32	32.0	7	9	US-09-805-761-63

16 32 32.0 9 16 US-10-600-187-78
17 32 32.0 12 14 US-10-247-946-4
18 32 32.0 12 14 US-10-251-526-4
19 32 32.0 13 9 US-09-795-006A-141
20 32 32.0 13 16 US-10-415-665-14
21 32 32.0 16 10 US-09-910-009A-454
22 32 32.0 17 12 US-10-362-527-115
23 32 32.0 17 12 US-10-362-527-156
24 31 31.0 10 9 US-09-779-308-461
25 31 31.0 11 12 US-10-435-238-21
26 31 31.0 11 12 US-09-784-553C-58
27 31 31.0 11 15 US-10-209-201C-58
28 31 31.0 15 10 US-09-932-613-67
29 31 31.0 15 10 US-09-932-322-67
30 31 31.0 16 9 US-09-777-710A-4
31 31 31.0 16 10 US-09-992-665-35
32 31 31.0 17 9 US-09-944-849-11
33 30 30.0 10 14 US-10-208-304-14
34 30 30.0 12 10 US-09-954-385-335
35 30 30.0 14 10 US-09-792-686A-10
36 30 30.0 14 13 US-10-139-841-9
37 30 30.0 14 13 US-10-014-485A-9
38 30 30.0 14 14 US-10-062-710-38
39 30 30.0 14 14 US-10-174-105A-9
40 30 30.0 15 9 US-09-829-549A-33
41 30 30.0 17 14 US-10-031-874A-158
42 29.5 29.5 17 10 US-09-226-157-26
43 29 29.0 10 10 US-09-833-203-58
44 29 29.0 13 14 US-10-007-521-102
45 29 29.0 13 14 US-10-007-521-104

ALIGNMENTS

RESULT 1
US-09-761-636A-8
; Sequence 8, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-8

Query Match 100.0%; Score 100; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCPPC 17
Db 1 CASELGKSTNTFCPPC 17

RESULT 2
US-09-761-636A-27
; Sequence 27, Application US/09761636A
; Patent No. US20020065218A1

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; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-28

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Query Match          93.0%; Score 93; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.7e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CASELGKSTNTFCCKPPC 17
Db 1 CASELGKSTNTFCCKPPC 17

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RESULT 5
US-09-761-636A-30
; Sequence 30, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
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; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-30

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Query Match          93.0%; Score 93; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.7e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CASELGKSTNTFCCKPPC 17
Db 1 CASELGKSTNTFCCKPPC 17

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RESULT 6
US-09-761-636A-32
; Sequence 32, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293

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; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-27

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Query Match          97.0%; Score 97; DB 9; Length 17;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
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QY 1 CASELGKSTNTFCCKPPC 17
Db 1 CASELGKSTNTFCCKPPC 17

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RESULT 3
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; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
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; SEQ ID NO 31
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; ORGANISM: synthetic construct
US-09-761-636A-31

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Best Local Similarity 94.1%; Pred. No. 9.2e-08;
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QY 1 CASELGKSTNTFCCKPPC 17
Db 1 CASELGKSTNTFCCKPPC 17

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RESULT 4
US-09-761-636A-28
; Sequence 28, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela

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; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-32

Query Match          93.0%; Score 93; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.7e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCPPC 17
Db 1 CASELGRSTNTFCPPC 17

RESULT 7
US-09-761-636A-29
; Sequence 29, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-29

Query Match          89.0%; Score 89; DB 9; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.5e-06;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CASDVGKSTNTWCKPPC 17

RESULT 8
US-09-761-636A-5
; Sequence 5, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-5

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Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 9
US-09-761-636A-15
; Sequence 15, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-15

Query Match          69.0%; Score 69; DB 9; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.0012;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CATELGKSTNTFC 13

RESULT 10
US-09-761-636A-16
; Sequence 16, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16
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Query Match 65.0%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.0049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CASELGKSTNTFC 13

RESULT 11
US-09-761-636A-18
; Sequence 18, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-18

Query Match 65.0%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.0049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
|||:|||||:
Db 1 CASELGKSTNTFC 13

RESULT 12
US-09-761-636A-17
; Sequence 17, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-17

Query Match 61.0%; Score 61; DB 9; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CASELGKSTNTFC 13

RESULT 13
US-10-435-238-22
; Sequence 22, Application US/10435238
; Publication No. US20030224972A1
; GENERAL INFORMATION:
; APPLICANT: HEARING, Vincent J., Jr.
; TITLE OF INVENTION: Depigmenting Activity of Agouti Signal Protein and Peptides Thereof
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: 127 Peachtree St., N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/435,238
; FILING DATE: 08-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,157
; FILING DATE: 22-Dec-1997
; APPLICATION NUMBER: PCT/US96/10695
; FILING DATE: 21 JUN 1996
; APPLICATION NUMBER: 60/ 000,436
; FILING DATE: 23 JUN 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 14014.0195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-435-238-22

Query Match 37.0%; Score 37; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 STNTFCKPP 16
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Db 1 ATNDSCKPP 9

RESULT 14
US-09-805-761-61
; Sequence 61, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkesh
; APPLICANT: Masood, Rizwan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; TITLE OF INVENTION: VEGF OLIGONUCLEOTIDES
; FILE REFERENCE: 21327-701CON2

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; CURRENT APPLICATION NUMBER: US/09/805,761
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-761-61

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Query Match          32.0%; Score 32; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9  TNTCKP 15
Db      1  TNTCKP 7

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RESULT 15
US-09-805-761-63
; Sequence 63, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkesh
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
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; SEQ ID NO 63
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-761-63

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Query Match          32.0%; Score 32; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9  TNTCKP 15
Db      1  TNTCKP 7

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Job time : 67 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:53:36 ; Search time 20 Seconds
(without alignments)
43.982 Million cell updates/sec

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCCKPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 157007

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	37.0	10	4	US-08-983-157B-22
2	32	32.0	9	4	US-09-644-600-78
3	32	32.0	9	4	US-09-654-600A-78
4	32	32.0	12	1	US-08-053-079A-4
5	32	32.0	12	2	US-08-685-589A-228
6	32	32.0	12	4	US-09-462-118-4
7	32	32.0	16	1	US-08-363-566-1
8	31	31.0	10	4	US-08-983-157B-21
9	31	31.0	16	3	US-09-328-501-4
10	31	31.0	16	4	US-09-777-710A-4
11	31	31.0	17	3	US-08-882-046-9
12	31	31.0	17	4	US-09-252-586-19
13	30	30.0	14	2	US-08-443-965B-9
14	30	30.0	14	2	US-08-425-989B-9
15	30	30.0	14	2	US-08-443-966B-9
16	30	30.0	14	3	US-08-853-910-3
17	30	30.0	14	4	US-09-148-712-13
18	29.5	29.5	15	1	US-08-487-485A-4
19	29.5	29.5	17	2	US-08-400-115-26
20	29	29.0	10	2	US-08-637-759B-408
21	29	29.0	10	3	US-08-871-355A-408
22	29	29.0	10	4	US-09-201-945-408
23	29	29.0	10	5	PCT-US96-01735-3
24	29	29.0	13	3	US-08-651-136C-102
25	29	29.0	13	3	US-08-651-136C-104
26	29	29.0	13	4	US-09-229-911A-102
27	29	29.0	13	4	US-09-229-911A-104

28 29 29.0 14 4 US-08-182-967-23 Sequence 23, Appl
29 29 29.0 15 1 US-07-689-693B-12 Sequence 12, Appl
30 29 29.0 15 3 US-09-230-222-3 Sequence 3, Appl
31 28.5 28.5 17 2 US-08-400-115-24 Sequence 24, Appl
32 28 28.0 9 3 US-09-258-754-63 Sequence 63, Appl
33 28 28.0 9 3 US-09-042-107-63 Sequence 63, Appl
34 28 28.0 9 4 US-09-722-250B-63 Sequence 11, Appl
35 28 28.0 10 5 PCT-US92-07865-11 Sequence 5, Appl
36 28 28.0 13 4 US-09-111-681C-5 Sequence 8, Appl
37 28 28.0 13 4 US-09-111-681C-8 Sequence 13, Appl
38 28 28.0 13 4 US-09-111-681C-13 Sequence 16, Appl
39 28 28.0 14 4 US-09-148-712-16 Sequence 16, Appl
40 28 28.0 15 4 US-09-947-372A-19 Sequence 19, Appl
41 28 28.0 17 1 US-08-141-892A-8 Sequence 8, Appl
42 28 28.0 17 1 US-08-141-892A-41 Sequence 41, Appl
43 28 28.0 17 2 US-08-583-447A-8 Sequence 8, Appl
44 28 28.0 17 2 US-08-583-447A-41 Sequence 41, Appl
45 28 28.0 17 2 US-08-583-447A-41 Sequence 41, Appl

ALIGNMENTS

RESULT 1

US-08-983-157B-22
; Sequence 22, Application US/08983157B
; Patent No. 6579848
; GENERAL INFORMATION:
; APPLICANT: HEARING, Vincent J., Jr.
; TITLE OF INVENTION: Depigmenting Activity of Agouti Signal Protein and Peptides Thereof
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Needle & Rosenberg, P.C.
; STREET: 127 Peachtree St., N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,157B
; FILING DATE: 22-Dec-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10695
; FILING DATE: 21 JUN 1996
; APPLICATION NUMBER: 60/ 000,436
; FILING DATE: 23 JUN 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 14014.0195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-983-157B-22

Query Match 37.0%; Score 37; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

us-09-761-636a-8.closed.ra1

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QY      8 STNFKCKP 16
      :||| |||||
Db      1 ATNDSCKP 9

RESULT 2
US-09-644-600-78
; Sequence 78, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotochi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 495-503 of the TADG-15 protein
US-09-644-600-78

Query Match      32.0%; Score 32; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 NTFCKP 15
      :||| |||||
Db      4 NKFCCKP 9

RESULT 3
US-09-654-600A-78
; Sequence 78, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotochi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 495-503 of the TADG-15 protein
US-09-654-600A-78

Query Match      32.0%; Score 32; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 NTFCKP 15
      :||| |||||
Db      4 NKFCCKP 9

RESULT 4
US-08-053-079A-4
; Sequence 4, Application US/08053079A
; Patent No. 5606026
; GENERAL INFORMATION:
; APPLICANT: Rodman
; APPLICANT: Natural Human Igm Antibodies
; TITLE OF INVENTION: 15
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dady & Darby
; STREET: 805 Third Ave.
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,079A
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph, R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 4436/16060US4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)527-7700
; TELEFAX: (212)753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Human immunodeficiency virus type 1
; IMMEDIATE SOURCE:
; CLONE: tat #4
US-08-053-079A-4

Query Match      32.0%; Score 32; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      9 TNTFCCKPPC 17
      :||| :|||
Db      2 TNCYCKKCC 10

RESULT 5
US-08-685-589A-228
; Sequence 228, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

```


STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 228:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..12
OTHER INFORMATION: /product= "Cyclic"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: /product= "Xaa=Caa=cyclohexylalanine"
US-08-685-589A-228

Query Match 32.0%; Score 32; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 FCKPFC 17
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DB 2 FCKPFC 7

RESULT 6
US-09-462-118-4
; Sequence 4, Application US/09462118
; Patent No. 6610833
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/09/462,118
; CURRENT FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-09-462-118-4

Query Match 32.0%; Score 32; DB 4; Length 12;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 TMTCKPFC 17
| | | |

Db 2 TNCYCKKC 10

RESULT 7

US-08-369-566-1
; Sequence 1, Application US/08369566
; Patent No. 5650151
; GENERAL INFORMATION:
; APPLICANT: Bausher, Michael G
; TITLE OF INVENTION: Citrus Proteins for Use in Field
; TITLE OF INVENTION: Detection of Citrus Blight Using Immunological Techniques
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: USDA-ARS
; STREET: Room 408, Bldg 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,566
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/792,508
; FILING DATE:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-344-1003
; TELEFAX: 301-344-5060
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-369-566-1

Query Match 32.0%; Score 32; DB 1; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GKSTNTCKPP 16
| : | | | |
DB 1 GEGTATFYTPP 11

RESULT 8

US-08-983-157B-21
; Sequence 21, Application US/08983157B
; Patent No. 6579848
; GENERAL INFORMATION:
; APPLICANT: HEARING, Vincent J., Jr.
; TITLE OF INVENTION: Depigmenting Activity of Agouti Signal
; Protein and Peptides thereof
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: 127 Peachtree St., N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

us-09-761-636a-8.closed.ra1

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,157B
; FILING DATE: 22-Dec-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10695
; FILING DATE: 21 JUN 1996
; APPLICATION NUMBER: 60/ 000,436
; FILING DATE: 23 JUN 1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 14014.0195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
;
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-983-157B-21

Query Match 31.0%; Score 31; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 STWTFCKPP 16
DB 1 ATRDSCKPP 9

RESULT 9
US-09-328-501-4
; Sequence 4, Application US/09328501A
; Patent No. 6258581
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. 6258581omu
; TITLE OF INVENTION: Ceramidase Gene
; FILE REFERENCE: 1422-0377P
; CURRENT APPLICATION NUMBER: US/09/328,501A
; CURRENT FILING DATE: 1999-06-09
; EARLIER APPLICATION NUMBER: 10-234769 JAPAN
; EARLIER FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; OTHER INFORMATION: any n or Xaa = Unknown
US-09-328-501-4

Query Match 31.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 SELGKSTNWF 12
DB 2 SEIGGSTRSF 11

RESULT 10
US-09-777-710A-4
; Sequence 4, Application US/09777710A
; Patent No. 6489117
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. 6489117omu et al.
;
; TITLE OF INVENTION: CERAMIDASE GENE
; FILE REFERENCE: 1422-0458P
; CURRENT APPLICATION NUMBER: US/09/777,710A
; CURRENT FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-777-710A-4

Query Match 31.0%; Score 31; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 SELGKSTNWF 12
DB 2 SEIGGSTRSF 11

RESULT 11
US-08-882-046-9
; Sequence 9, Application US/08882046
; Patent No. 6136952
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; APPLICANT: Hood, Leroy
; APPLICANT: Krantz, Ian D. B.
; APPLICANT: Spinner, Nancy B.
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,046
; FILING DATE: 25-JUN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UW 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-882-046-9

Query Match 31.0%; Score 31; DB 3; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GKSTNTFCCK 15
DB 7 GFGCNKFCKP 16

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RESULT 12

US-09-252-586-19
 ; Sequence 19, Application US/09252586
 ; Patent No. 6387643
 ; GENERAL INFORMATION:
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Fairbanks, Michael B.
 ; APPLICANT: Milner, Ana M.
 ; TITLE OF INVENTION: Human Platelet Heparanase Polypeptides,
 ; TITLE OF INVENTION: Polynucleotide Heparanase That Encode Them, and Methods For
 ; TITLE OF INVENTION: the Identification of Compounds That Alter Heparanase
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pharmacia & Upjohn
 ; STREET: 301 Henrietta
 ; CITY: Kalamazoo
 ; STATE: MI
 ; COUNTRY: USA
 ; ZIP: 49001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/09/252,586
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kerber, Lori L.
 ; REGISTRATION NUMBER: 41,113
 ; REFERENCE/DOCKET NUMBER: 6131.N CN1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 616-833-0974
 ; TELEFAX: 616-833-8897
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; US-09-252-586-19

Query Match 31.0%; Score 31; DB 4; Length 17;
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 ELGKSTNTPCK 14
 Db ||| |||
 7 ELGNEPNSFLK 17

RESULT 13

US-08-443-965B-9
 ; Sequence 9, Application US/08443965B
 ; Patent No. 5821341
 ; GENERAL INFORMATION:
 ; APPLICANT: McClelland, Alan
 ; APPLICANT: Greve, Jeffrey M.
 ; TITLE OF INVENTION: Soluble Molecule Related to but
 ; TITLE OF INVENTION: Distinct from ICAM-1
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bayer Corporation
 ; STREET: 400 Morgan Lane
 ; CITY: West Haven
 ; STATE: Connecticut
 ; COUNTRY: USA
 ; ZIP: 06516
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" diskette, 1.44 MB storage

; COMPUTER: IBM Thinkpad 760ED
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: WordPerfect 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/443,965B
 ; FILING DATE: 18-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/425,989
 ; FILING DATE: 20-APR-1995
 ; APPLICATION NUMBER: 08/156,653
 ; FILING DATE: 22-NOV-1993
 ; APPLICATION NUMBER: 08/005,204
 ; FILING DATE: 15-JAN-1993
 ; APPLICATION NUMBER: 07/449,356
 ; FILING DATE: 21-DEC-1989
 ; APPLICATION NUMBER: 07/445,951
 ; FILING DATE: 13-DEC-1989
 ; APPLICATION NUMBER: 07/301,192
 ; FILING DATE: 24-JAN-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barbara A. Shimei
 ; REGISTRATION NUMBER: 29,862
 ; REFERENCE/DOCKET NUMBER: MTI 209.2C3D2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (203) 812-2786
 ; TELEFAX: (203) 812-5492
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acid residues
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: no
 ; FRAGMENT TYPE: C-terminal fragment
 ; FEATURE:
 ; NAME/KEY: modified ICAM fragment
 ; LOCATION: C-terminus
 ; OTHER INFORMATION: first 11 amino acid
 ; OTHER INFORMATION: residues correspond to the C-terminus of
 ; OTHER INFORMATION: ICAM; last residue (Cys) added to facilitate
 ; OTHER INFORMATION: coupling
 ; US-08-443-965B-9

Query Match 30.0%; Score 30; DB 2; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NTFCKPCC 17
 Db ||| |||
 7 NTQATPPC 14

RESULT 14

US-08-425-989B-9
 ; Sequence 9, Application US/08425989B
 ; Patent No. 5849699
 ; GENERAL INFORMATION:
 ; APPLICANT: McClelland, Alan
 ; APPLICANT: Greve, Jeffrey M.
 ; TITLE OF INVENTION: Soluble Molecule Related to but
 ; TITLE OF INVENTION: Distinct from ICAM-1
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bayer Corporation
 ; STREET: 400 Morgan Lane
 ; CITY: West Haven
 ; STATE: Connecticut
 ; COUNTRY: USA
 ; ZIP: 06516
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" diskette, 1.44 MB storage
 ; COMPUTER: IBM Thinkpad 760ED

```
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,989B
FILING DATE: 20-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/156,653
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 08/005,204
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: 07/449,356
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: 07/445,951
FILING DATE: 13-DEC-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 24-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Barbara A. Shimei
REGISTRATION NUMBER: 29,862
REFERENCE/DOCKET NUMBER: MTI 209.203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2786
TELEFAX: (203) 812-5492
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: C-terminal fragment
FEATURE:
NAME/KEY: modified ICAM fragment
LOCATION: C-terminus
OTHER INFORMATION: first 11 amino acid
OTHER INFORMATION: residues correspond to the C-terminus of
OTHER INFORMATION: ICAM; last residue (Cys) added to facilitate
OTHER INFORMATION: coupling
US-08-425-989B-9
Query Match 30.0%; Score 30; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 NTFCKPPC 17
Db 7 NTQATPPC 14
RESULT 15
US-08-443-966B-9
Sequence 9, Application US/08443966B
Patent No. 5859212
GENERAL INFORMATION:
APPLICANT: McClelland, Alan
APPLICANT: Greve, Jeffrey M.
TITLE OF INVENTION: Soluble Molecule Related to but
TITLE OF INVENTION: Distinct from ICAM-1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB storage
COMPUTER: IBM ThinkPad 760D
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/443,966B
FILING DATE: 18-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/425,989
FILING DATE: 20-APR-1995
APPLICATION NUMBER: 08/156,653
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 08/005,204
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: 07/449,356
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: 07/445,951
FILING DATE: 13-DEC-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 24-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Barbara A. Shimei
REGISTRATION NUMBER: 29,862
REFERENCE/DOCKET NUMBER: MTI 209.2C3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2786
TELEFAX: (203) 812-5492
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: C-terminal fragment
FEATURE:
NAME/KEY: modified ICAM fragment
LOCATION: C-terminus
OTHER INFORMATION: first 11 amino acid
OTHER INFORMATION: residues correspond to the C-terminus of
OTHER INFORMATION: ICAM; last residue (Cys) added to facilitate
OTHER INFORMATION: coupling
US-08-443-966B-9
Query Match 30.0%; Score 30; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 NTFCKPPC 17
Db 7 NTQATPPC 14
Search completed: September 5, 2004, 10:56:57
Job time : 21 secs
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:00:28 ; Search time 11.6667 Seconds
(without alignments)
74.205 Million cell updates/sec

Title: US-09-761-636A-9

Perfect score: 55

Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	24	43.6	9	2	C24180		fibrinogen beta ch
2	19	34.5	8	2	PC1002		leucine-tRNA ligas
3	18	32.7	6	4	I79564		hypothetical TCU3
4	18	32.7	9	2	D24180		fibrinogen beta ch
5	18	32.7	9	2	PH0942		T-cell receptor be
6	17	30.9	6	2	S29637		jacalin beta-II ch
7	17	30.9	6	2	I37263		Y protein - human
8	17	30.9	7	2	PH0932		T-cell receptor be
9	17	30.9	9	2	D28854		fibrinopeptide B -
10	17	30.9	9	2	E28854		fibrinopeptide B -
11	17	30.9	9	2	F28854		fibrinopeptide B -
12	16	29.1	9	2	PH0935		T-cell receptor be
13	16	29.1	9	2	PH0921		T-cell receptor be
14	15	27.3	6	2	JU0355		lipopeptide WS1279
15	15	27.3	7	2	B39040		calsequestrin, fas
16	15	27.3	8	2	S59622		metallothionein is
17	15	27.3	8	2	S19288		acylase - Kluyvera
18	15	27.3	8	2	S69165		ferredoxin a2 - Ja
19	15	27.3	9	2	A11497		transaldolase (EC
20	15	27.3	9	2	A26363		cardioactive pepti
21	15	27.3	9	2	S27233		cardioactive pepti
22	15	27.3	9	2	PH0917		cardioactive pepti
23	15	27.3	9	2	S39767		T-cell receptor be
24	14	25.5	6	2	B31263		cardioactive pepti
25	14	25.5	6	2	S29881		dihydrofolate redu
26	14	25.5	7	1	KEYDGD		Na+/K+-exchanging
27	14	25.5	8	2	B47594		galactose oxidase
28	14	25.5	9	2	A61230		aspartate kinase
29	14	25.5	9	2	B39504		calsequestrin, car
							octamer-binding pr

ALIGNMENTS

RESULT 1

C24180

fibrinogen beta chain - Japanese macaque (fragment)

N:Contains: fibrinopeptide B

C:Species: Macaca fuscata (Japanese macaque)

C>Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996

C/Accession: C24180

R:Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 97, 1487-1492, 1985

A>Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E

uonens, and baboons.

A/Reference number: A91990; MUID:85289140; PMID:3928610

A/Accession: C24180

A/Molecule type: protein

A/Residues: 1-9 <NAK>

C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

Query Match 43.6%; Score 24; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NEESL 7

Db 1 NEESL 5

RESULT 2

PC1002

leucine-tRNA ligase (EC 6.1.1.4) - Escherichia coli (fragments)

N/Alternate names: leucyl-tRNA synthetase

C/Species: Escherichia coli

C/Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 03-Jun-2002

C/Accession: PC1002

R:Miao, F.; Shi, J.P.; Wang, Y.L.

Science in China (series B) 34, 691-698, 1991

A/Title: Chemical modification of sulphydryl groups of E. coli leucyl-tRNA synthetase an

A/Reference number: PC1002

A/Accession: PC1002

A/Molecule type: protein

A/Residues: 1-8 <MIA>

C/Comment: This enzyme catalyzes the aminoacylation of tRNA(Leu) with Leucine.

C/Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

F;5-8/Region: catalytic #status predicted

Query Match 34.5%; Score 19; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCN 3

Db 4 CCD 6

```
RESULT 3
I79564
hypothetical TCL3 protein (mistranslated) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
C:Accession: I79564
R:Zurter, M.; Hockett, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.C.;
Proc. Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990
A>Title: The t(10;14)(q24;q11) of T-cell acute lymphoblastic leukemia juxtaposes the del
A:Reference number: 159162; MUID:90222189; PMID:2326274
C:Accession: I79564
A:Accession: I79564
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <ZUT>
A:CROSS-references: GB:M33602; NID:g339907; PIDN:AAA66449.1; PID:g807656
C:Comment: This is the hypothetical translation of a sequence translated in an incorrect
Query Match 32.7%; Score 18; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CC 2
Db 3 CC 4
RESULT 4
D24180
fibrinogen beta chain - red guenon (fragment)
N/Contains: fibrinopeptide B
C:Species: Erythrocybus patas (red guenon, hussar)
C>Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C:Accession: D24180
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A>Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (B
uonens, and baboons.
A:Reference number: A91990; MUID:85289140; PMID:3928610
A:Accession: D24180
A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
Query Match 32.7%; Score 18; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 NEESL 7
Db 1 NEEVL 5
RESULT 5
PH0342
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0342
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerg
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0942
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A>Note: the authors translated the codon TGC for residue 2 as Ala
C:Keywords: T-cell receptor
Query Match 32.7%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CC 2
Db 1 CC 2
RESULT 6
S29637
Jacalin beta-II chain - Artocarpus champeden (fragment)
C:Species: Artocarpus champeden
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C:Accession: S29637
R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.
Biochim. Biophys. Acta 1156, 219-222, 1993
A>Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD
A:Reference number: S29635; MUID:93152601; PMID:8427879
A:Accession: S29637
A:Molecule type: protein
A:Residues: 1-6 <NGO>
A:Experimental source: seed
A:Complex: heterotetramer; two alpha and two beta chains
C:Function:
A:Description: seed storage protein
A>Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine
C:Keywords: heterotetramer; lectin; seed; storage protein
Query Match 30.9%; Score 17; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 NEES 6
Db 1 NEQS 4
RESULT 7
I37263
Y protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: I37263
R:Waeber, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A>Title: Novel testis germ cell-specific transcript of the CREB gene contains an altern
A:Reference number: I37263; MUID:93010691; PMID:1396344
A:Accession: I37263
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:CROSS-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C:Genetics:
A:Gene: CREB
Query Match 30.9%; Score 17; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 SLIC 9
Db 1 SLFC 4
RESULT 8
PH0932
T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0932
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0932
```

A:Molecule type: mRNA
A:Residues: 1-7 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
C:Keywords: T-cell receptor

Query Match 30.9%; Score 17; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCNEESL 7
| : |
Db 1 CASPERL 7

RESULT 9

F28854
fibrinopeptide B - olive baboon
C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Aug-2000
C:Accession: D28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: D28854
A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.9%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEESL 7
| : |
Db 1 NOEGL 5

RESULT 10

E28854
fibrinopeptide B - hamadryas baboon
C:Species: Papio hamadryas (hamadryas baboon)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Aug-2000
C:Accession: E28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: E28854
A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.9%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEESL 7
| : |
Db 1 NOEGL 5

RESULT 11

F28854
fibrinopeptide B - gelada baboon
C:Species: Theropithecus gelada (gelada baboon)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Aug-2000
C:Accession: F28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: F28854

A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.9%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEESL 7
| : |
Db 1 NOEGL 5

RESULT 12

PH0935
T-cell receptor beta chain V-D-J region (clone 6) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0935
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic arthritis
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0935
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
C:Keywords: T-cell receptor

Query Match 29.1%; Score 16; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6
| : |
Db 1 CASSET 6

RESULT 13

PH0921
T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0921
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic arthritis
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0921
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
C:Keywords: T-cell receptor

Query Match 29.1%; Score 16; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6
| : |
Db 1 CASSEN 6

RESULT 14

JU0355
lipopeptide WS1279 [validated] - Streptomyces willmorei
C:Species: Streptomyces willmorei
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: JU0355
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A:Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin
A:Reference number: JU0355; MUID:91300586; PMID:2070441

A:Accession: JU0355
A:Molecule type: protein
A:Residues: 1-6 <FSU>
A:Note: the structure was confirmed by synthesis
C:Keywords: blocked amino end; lipoprotein
F:/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F:/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 27.3%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CN 3
|||
DB 1 CN 2

RESULT 15
B39040
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C:Accession: B39040
R:Calla, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein
A:Reference number: A39040; MUID:91093153; PMID:1985907
A:Accession: B39040
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <CAL>
C:Keywords: phosphoprotein; skeletal muscle

Query Match 27.3%; Score 15; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEESL 7
:|:
DB 2 DEEDL 6

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:57:02 ; Search time 7 Seconds
(without alignments)
66.947 Million cell updates/sec

Title: US-09-761-636A-9
Perfect score: 55
Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	24	43.6	9	1 FIBB MACFU	P19346 macaca fusc
2	18	32.7	9	1 FIBB ERYPA	P19346 erythrocebu
3	17	30.9	9	1 FIBB PAPAN	P19344 papio anubi
4	17	30.9	9	1 FIBB PAPHA	P19343 papio hamad
5	17	30.9	9	1 FIBB THEGE	P19342 theropithec
6	16	29.1	9	1 ULAK MOUSE	P99031 mus musculu
7	15	27.3	9	1 CCAP CARMA	P38556 carcinus ma
8	15	27.3	9	1 TAL3 PICJA	P17441 picchia jadi
9	14	25.5	7	1 IGAO DACDE	P06294 dactylium d
10	13	23.6	5	1 TRM3 ECOLI	P13973 escherichia
11	13	23.6	8	1 PLP BRANA	P81707 brassica na
12	13	23.6	9	1 SAME MUSCA	P19095 mustelus ca
13	12	21.8	7	1 UF03 MOUSE	P38641 mus musculu
14	12	21.8	8	1 UP41 HUMAN	P30087 homo sapien
15	12	21.8	9	1 SAP STOVA	P24047 stomopneute
16	12	21.8	9	1 TAL1 PICJA	P17440 picchia jadi
17	11	20.0	7	1 BRHP CONIM	P58803 conus imper
18	11	20.0	7	1 FARI ASCSU	P31889 ascaris suu
19	11	20.0	8	1 CADI ENTFA	P13268 enterococcu
20	11	20.0	9	1 RT33 BOVIN	P82926 bos taurus
21	11	20.0	9	1 UP47 HUMAN	P30093 homo sapien
22	10	18.2	8	1 ACT CARMA	P80709 carcinus ma
23	10	18.2	9	1 FAR4 CALVO	P41859 calliphora
24	10	18.2	9	1 OXYT BUFRE	F42995 bufo regula
25	9	16.4	6	1 TMOF SARBU	P41495 sarcophaga
26	9	16.4	8	1 COW2 CONPU	P58785 conus purpu
27	9	16.4	8	1 GLUR HUMAN	P02729 homo sapien
28	9	16.4	9	1 CONO CONGE	P05486 conus geogr
29	9	16.4	9	1 CONO CONST	P05487 conus stria
30	9	16.4	9	1 COW CONVE	P83047 conus ventr
31	9	16.4	9	1 DNFI LOOMI	P16339 locusta mig
32	9	16.4	9	1 ISOT CYPCA	P42993 cyprinus ca
33	9	16.4	9	1 MGMT_BOVIN	P29177 bos taurus

34	9	16.4	9	1 OXYA_SCYCA	P42996 scylliorhinu
35	9	16.4	9	1 OXYA_SQUAC	P42999 squalus aca
36	9	16.4	9	1 OXYF_SCYCA	P42997 scylliorhinu
37	9	16.4	9	1 OXYT_CYPCA	P23879 cyprinus ca
38	9	16.4	9	1 OXYT_EISFO	P23998 eisenia foe
39	9	16.4	9	1 OXYT_OCTVU	P80027 octopus vul
40	9	16.4	9	1 OXYT_RABIT	P32878 oryctolagus
41	9	16.4	9	1 OXYT_RAUCL	P42994 raja clavav
42	9	16.4	9	1 OXYV_SQUAC	P43000 squalus aca
43	9	16.4	9	1 UF02_MOUSE	P38640 mus musculu
44	9	16.4	9	1 UN19_CLOPA	P81355 clostridium
45	8	14.5	6	1 ACPH_RABIT	P25154 oryctolagus

ALIGNMENTS

RESULT 1
FIBB MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;

Query Match 43.6%; Score 24; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NEESL 7
Db 1 NEESL 5

RESULT 2
FIBB ERYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons."
RL J. Biochem. 97:1487-1492 (1985).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; D24180; D24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 32.7%; Score 18; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NEESL 7
Db 1 NEEVL 5

RESULT 3
FIBB PAPAN
ID FIBB PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons."
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; D24180; D24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 32.7%; Score 18; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NEESL 7
Db 1 NEEVL 5

RESULT 3
FIBB PAPAN
ID FIBB PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons."
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.

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DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDFE6409C7287B06 CRC64;

Query Match 30.9%; Score 17; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NEESL 7
Db 1 NQEGL 5

RESULT 4
FIBB PAPA
ID FIBB PAPA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons."
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; E28854; E28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1057 MW; DDFE71B9C7287B06 CRC64;

Query Match 30.9%; Score 17; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NEESL 7
Db 1 NQEGL 5

RESULT 5
FIBB THEGE
ID FIBB THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).

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GN FGB.
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Theropithecus.
OX NCBI_TaxID=9565;
RN [1]
RN SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PFM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; F28854; F28854.
DR InterPro; IPR002181; Fibrinogen.C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 1 9
SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;
Query Match 30.9%; Score 17; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 NEESL 7
|:|
Db 1 NOEGL 5
RESULT 6
ULAK_MOUSE STANDARD; PRT; 9 AA.
ID ULAK_MOUSE
AC P99031;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE.
RP TISSUE=Liver;
RC Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA Cowthorne M.;
RL Submitted (AUG-1998) to Swiss-Prot.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.0, its MW is: 12.5 kDa.
DR SWISS-2DPAGE; P99031; MOUSE.
FT NON TER 9
SQ SEQUENCE 9 AA; 1106 MW; E1E842C3240B145A CRC64;
Query Match 29.1%; Score 16; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 NEESL 8
|:|
Db 3 NERKVI 8

RESULT 7
CCAP_CARMA STANDARD; PRT; 9 AA.
ID CCAP_CARMA
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunodea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RN SEQUENCE.
RP SPECIES=C.maenas; TISSUE=Pericardial organs;
RC Stangler J., Hilbich C., Beyreuther K., Keller R.;
RA "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).
RN [2]
RN SEQUENCE.
RP SPECIES=M.sexta;
RC MEDLINE=93050243; PubMed=1426284;
RX Cheung C.-C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RA "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168 (1992).
RN [3]
RN SEQUENCE.
RP SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RC MEDLINE=94176032; PubMed=8129851;
RX Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).
CC -!- FUNCTION: The effect of CCAP is both ino- and chronotropic.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Stored in pericardial organs and released
CC into the hemolymph.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;
Query Match 27.3%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CN 3
|
Db 3 CN 4
RESULT 8
TAL3_PICUA STANDARD; PRT; 9 AA.
ID TAL3_PICUA
AC P17441;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transaldolase III (EC 2.2.1.2) (Fragment).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.

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OX NCBI_TaxID=4903;
RN [1]
RP SEQUENCE.
RX MEDLINE=75145197; PubMed=1092268;
RA Tsolas O., Sun S.C.;
RT "Isolation of a peptide containing a histidyl-cysteiny sequence
RT from the active center of transaldolase.";
RL Arch. Biochem. Biophys. 167:525-533(1975).
CC -!- FUNCTION: Transaldolase is important for the balance of
CC metabolites in the pentose-phosphate pathway.
CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.
DR PIR; A11497; A11497.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CN 3
Db |||
5 CN 6

RESULT 9
IGAO DACDE
ID IGAC DACDE STANDARD; PRT; 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
OX NCBI_TaxID=5132;
RN [1]
RP SEQUENCE.
RA Avigad G., Markus Z.;
RT "Identification of a peptide inhibitor of galactose oxidase from
RT Dactylium dendroides.";
RL Fed. Proc. 31:447-447(1972).
CC -!- FUNCTION: Binds one copper ion per molecule but does not bind the
CC galactose oxidase apoenzyme. It may inactivate the enzyme by
CC binding to its prosthetic copper group.
DR PIR; A01341; XEYDGD.
KW Copper; Metalloenzyme inhibitor.
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEES 6
Db |||
4 NTES 7

RESULT 10
TRM3_ECOLI
ID TRM3_ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Tram protein (Fragment).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traJ
RT and traY genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the traM family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL; M20941; -; NOT ANNOTATED CDS.
DR PIR; A32014; A32014.
KW Conjugation; Plasmid; DNA-binding.
FT NON_TER 1
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NEES 5
Db |||
2 NDE 4

RESULT 11
PLP_BRANA
ID PLP_BRANA STANDARD; PRT; 8 AA.
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DB Plastidial lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RX STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planta 208:588-598(1999).
CC -!- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC specific plastidial lipid organelle.
CC -!- TISSUE SPECIFICITY: Tapetum of anthers.
FT NON_TER 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

CC
-!
MISCELLANEOUS:
On the 2D-gel the determined pI of this unknown protein is: 5.1, its MW is: 36 kDa.
NON TER
7
CC
FT
TT
CN
CC
CC
F-! FUNCTION: Cause stimulation of sperm respiration and motility through intracellular alkalization, transient elevations of pH
RZES DETC. 2941879-102A(1997)
KL

CC CAMP, cGMP and calcium levels in sperm cells, and transient
CC activation and subsequent inactivation of the membrane form of
CC guanylate cyclase.

FT DISULFID 3

SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;

Query Match

Best Local Similarity 21.8%; Score 12; DB 1; Length 9;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CNE 4

Db 3 CPE 5

Search completed: September 5, 2004, 11:04:00

Job time : 7 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:59:47 ; Search time 31.6667 Seconds
(without alignments)
89.674 Million cell updates/sec

Title: US-09-761-636A-9

Perfect score: 55

Sequence: 1 CCNRESLIC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	32.7	8	Q8IV87	Q8IV87 homo sapien
2	18	32.7	8	Q9SAY7	Q9SAY7 dioscorea t
3	18	32.7	9	Q9FSZ2	Q9FSZ2 cicor ariet
4	18	32.7	9	Q8CG13	Q8CG13 mus musculus
5	18	32.7	9	Q9EIU7	Q9EIU7 hepatitis b
6	17	30.9	9	Q86SF0	Q86SF0 homo sapien
7	16	29.1	7	Q67113	Q67113 influenzavi
8	16	29.1	7	Q42564	Q42564 fugu rubrip
9	15	27.3	9	P82440	P82440 nicotiana t
10	15	27.3	9	O12096	O12096 caprine art
11	15	27.3	9	O12100	O12100 caprine art
12	15	27.3	9	O12102	O12102 caprine art
13	15	27.3	9	O12098	O12098 caprine art
14	15	27.3	9	O12104	O12104 caprine art
15	14	25.5	9	Q8MJT7	Q8MJT7 eulemur ful
16	14	25.5	9	Q8MJT8	Q8MJT8 eulemur ful

17	23.6	7	11	O55184	O55184 rattus norv
18	23.6	8	2	O32560	O32560 escherichia
19	23.6	8	11	P70243	P70243 mus musculus
20	23.6	9	6	Q9TUY0	Q9TUY0 monodelphis
21	23.6	9	11	Q8CG39	Q8CG39 rattus norv
22	21.8	7	13	Q8J320	Q8J320 gallus gall
23	21.8	8	2	Q9ZEZ9	Q9ZEZ9 buchnera ap
24	21.8	8	4	Q9BYV5	Q9BYV5 homo sapien
25	21.8	8	4	O15895	O15895 homo sapien
26	21.8	8	4	O15890	O15890 homo sapien
27	21.8	8	6	Q9BF82	Q9BF82 ursus arcto
28	21.8	8	6	Q9BF82	Q9BF82 macropus eu
29	21.8	8	6	Q9BF90	Q9BF90 tragelaphus
30	21.8	8	6	Q9BF81	Q9BF81 echinops te
31	21.8	8	6	Q9BF93	Q9BF93 megaptera n
32	21.8	8	6	Q9BF81	Q9BF81 atelies fusc
33	21.8	8	6	Q9BF87	Q9BF87 tapirus ind
34	21.8	8	6	Q9BF89	Q9BF89 euphractus
35	21.8	8	6	Q9BF88	Q9BF88 chaetophrac
36	21.8	8	6	Q9BFA0	Q9BFA0 macaca mula
37	21.8	8	6	Q9BFA8	Q9BFA8 loxodonta a
38	21.8	8	6	Q9BFA9	Q9BFA9 procavia ca
39	21.8	8	6	Q9BF82	Q9BF82 sorex arane
40	21.8	8	6	Q9BF85	Q9BF85 erinaceus c
41	21.8	8	6	Q9BF86	Q9BF86 myrmecophag
42	21.8	8	6	Q9BF83	Q9BF83 condylura c
43	21.8	8	6	Q9BF88	Q9BF88 equus cabal
44	21.8	8	6	Q9BF95	Q9BF95 roussetus l
45	21.8	8	6	Q9BF99	Q9BF99 hylobates c

ALIGNMENTS

RESULT 1
Q8IV87 PRELIMINARY; PRT; 8 AA.
AC Q8IV87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE DJ107712.2 (Serine palmitoyltransferase, long chain base subunit
2-like (Aminotransferase 2), variant 1) (Fragment).
GN SPTLC2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050320; CAD54807.1; -;
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 308 MW; 8E533682CEBEB042 CRC64;
Query Match 32.7%; Score 18; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CC 2
Db 3 CC 4
RESULT 2
Q9SAY7 PRELIMINARY; PRT; 8 AA.
ID Q9SAY7
AC Q9SAY7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Phosphoglucose isomerase (Fragment).
DS Diocoreea tokoro.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;
OC Diocoreea.
CX NCBI_TaxID=64475;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DT17-1;
RX MEDLINE=20279211; PubMed=10821191;
RA Terauchi R., Kahl G.;
RT "Rapid isolation of promoter sequences by TAIL-PCR: the 5'-flanking
RL regions of Pal and Pgi genes from yams (Dioscorea).";
EL Mol. Gen. Genet. 263:554-560(2000).
DR EMBL; AB016716; BAA32235.1; -.
DR GO; GO:0016853; P:isomerase activity; IEA.
FT NON TER
KW Isomerase.
SQ SEQUENCE 8 AA; 839 MW; F7B05731B5A1ADD6 CRC64;

Query Match 32.7%; Score 18; DB 10; Length 8;
Best Local Similarity 75.0%; Pred.No.1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLIC 9
Db 5 TLIC 8

RESULT 3
Q9FSZ2 PRELIMINARY; PRT; 9 AA.
AC Q9FSZ2
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Cicer arietinum (Chickpea) (Garbanzo).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
CX NCBI_TaxID=3827;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Castellana; TISSUE=Etisolated epicotyl;
RA Dopic B., Jimenez T., Labrador E.;
RT "cDNA clones expressed in etiolated Cicer arietinum epicotyls.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ299069; CAC10216.1; -.
DR EMBL; AJ299069; CAC10216.1; -.
KW Hypothetical protein.
FT NON TER
KW 1
SQ SEQUENCE 9 AA; 990 MW; 9441BDDAA7272EBE CRC64;

Query Match 32.7%; Score 18; DB 10; Length 9;
Best Local Similarity 100.0%; Pred.No.1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CC 2
Db 1 CC 2

RESULT 4
Q8CG13 PRELIMINARY; PRT; 9 AA.
AC Q8CG13;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A
DE (Fragment).
EN GRIN11A.

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22630144; PubMed=12745064;
RA Chew C.H., Samian M.R., Najimudin N., Tengku Muhammad T.S.;
RT "Molecular characterisation of six alternatively spliced variants and
a novel promoter in human peroxisome proliferator-activated receptor
alpha.";
RL Biochem. Biophys. Res. Commun. 305:235-243 (2003).
DR EMBL; AY258326; AAO89521.1; -.
DR EMBL; AY258327; AAO89522.1; -.
DR EMBL; AY258328; AAO89523.1; -.
DR EMBL; AY258329; AAO89524.1; -.
DR EMBL; AY258330; AAO89525.1; -.
DR EMBL; AY258331; AAO89526.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
KW Receptor.
FT NON_TER
SQ SEQUENCE 9 AA; 994 MW; DF8E3775BB01AAB2 CRC64;

Query Match 30.9%; Score 17; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ESLIC 9
DB 5 ESPLC 9

RESULT 7
Q67113 PRELIMINARY; PRT; 7 AA.
AC Q67113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3' end
DE (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922;
RA Dhar R., Chanock R.M., Lai C.-J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
FT NON_TER
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 29.1%; Score 16; DB 12; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 CNEESLIC 9
DB 3 CN----IC 6

RESULT 8
O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
DR GO; GO:0005216; F-ion channel activity; IEA.
KW Ionic channel.
FT NON_TER
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 29.1%; Score 16; DB 13; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 LIC 9
DB 3 LVC 5

RESULT 9
P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 42 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON_TER
SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2DSBB1B07 CRC64;

Query Match 27.3%; Score 15; DB 10; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EESL 7
DB 3 EESV 6

RESULT 10
O12096 PRELIMINARY; PRT; 9 AA.
AC O12096;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.

```

```

OS  Caprine arthritis encephalitis virus (CAEV).
OC  Viruses; Retroviridae; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11660;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT  "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RL  to A substitutions.";
DR  Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U81439; AAB60832.1; -.
FT  NON_TER 1
SQ  SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match      27.3%; Score 15; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CN 3
Db  ||
   6 CN 7

RESULT 11
O12100 PRELIMINARY; PRT; 9 AA.
AC O12100;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RL to A substitutions.";
DR Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81441; AAB60836.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match      27.3%; Score 15; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CN 3
Db  ||
   6 CN 7

RESULT 12
O12102 PRELIMINARY; PRT; 9 AA.
AC O12102;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RL to A substitutions.";
DR Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81442; AAB60838.1; -.
FT NON_TER 1

```

```

SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match      27.3%; Score 15; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CN 3
Db  ||
   6 CN 7

RESULT 13
O12098 PRELIMINARY; PRT; 9 AA.
AC O12098;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RL to A substitutions.";
DR Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81440; AAB60835.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match      27.3%; Score 15; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CN 3
Db  ||
   6 CN 7

RESULT 14
O12104 PRELIMINARY; PRT; 9 AA.
AC O12104;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RL to A substitutions.";
DR Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81443; AAB60840.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;

Query Match      27.3%; Score 15; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CN 3
Db  ||
   6 CN 7

```

```
RESULT 15
Q8MJT7 PRELIMINARY; PRT; 9 AA.
ID Q8MJT7
AC Q8MJT7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hemopexin (Fragment).
OS Eulemur fulvus (brown lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Eulemur.
OX NCBI_TaxID=13515;
RN [1]
RP SEQUENCE FROM N.A.
RA Wyner Y.M., Johnson S.E., Stumpf R., DeSalle R.;
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
RT zone at Andringitra, Madagascar."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258049; AAM43870.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;

Query Match 25.5%; Score 14; DB 6; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 EESLI 8
Db |||
2 ERGIL 6
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Search completed: September 5, 2004, 11:05:41
Job time : 32.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:56:37 ; Search time 37.3333 Seconds
(without alignments)
68.114 Million cell updates/sec

Title: US-09-761-636A-9

Perfect score: 55

Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 231240

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	4	AAU04528
2	50	90.9	9	4	AAU04552
3	49	89.1	9	4	AAU04553
4	46	83.6	8	4	AAU04525
5	43	78.2	8	4	AAU04539
6	42	76.4	8	4	AAU04541
7	41	74.5	8	4	AAU04538
8	39	70.9	8	4	AAU04540
9	35	63.6	8	4	AAU08451
10	33	60.0	8	4	AAU08460
11	33	60.0	9	6	ABR29819
12	33	60.0	9	6	ABR28797
13	33	60.0	9	6	ABR29456
14	33	60.0	9	6	ABR28814
15	33	60.0	9	6	ABR29789
16	33	60.0	9	6	ABR28619
17	33	60.0	9	6	ABR29608
18	33	60.0	9	6	ABR29220
19	33	60.0	9	6	ABR29572
20	33	60.0	9	6	ABR29383
21	31	56.4	6	2	AAK93979
22	30	54.5	8	2	AAK24954
23	30	54.5	8	3	AAy54526
24	29	52.7	9	6	ABR28842
25	28	50.9	9	2	AAW09329

26	28	50.9	9	2	AAy47045
27	28	50.9	9	6	ABR28618
28	28	50.9	9	6	ABR29242
29	27	49.1	8	2	AAr47420
30	27	49.1	8	2	AAr47390
31	27	49.1	8	2	AAr47421
32	27	49.1	8	2	AAr47419
33	27	49.1	9	2	AAW09330
34	27	49.1	9	5	ABG99560
35	26	47.3	8	2	AAr73351
36	26	47.3	8	2	AAr73350
37	26	47.3	8	3	AAy87160
38	26	47.3	8	3	AAy57040
39	26	47.3	8	4	AAE06137
40	26	47.3	8	5	ABG33960
41	26	47.3	9	2	AAr55115
42	26	47.3	9	2	AAW09328
43	26	47.3	9	2	AAW60376
44	26	47.3	9	2	AAW93702
45	26	47.3	9	2	AAy48648

ALIGNMENTS

RESULT 1
AAU04528
ID AAU04528 standard; protein; 9 AA.

XX AAU04528;

DT 26-SEP-2001 (first entry)

DE VEGF based bicyclic dimeric peptide #2.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1 /note= "A disulfide bond forms between residue 1 and residue 1 of an identical peptide to form a dimeric peptide, or between residue 1 and residue 17 of the sequence appearing as AAU04527 also forming a dimeric peptide"

FT Disulfide-bond 2..9 /note= "This bond cyclises the peptide"

WO200152875-A1.

26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P.

16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES.

PI Achen MG, Hughes RA, Stacker S, Cendron A;

WPI; 2001-442248/47.

PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

XX Claim 59; Page 32; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCNEESLIC 9
 |||||
 Db 1 CCNEESLIC 9
 |||||
 RESULT 2
 AAU04552
 ID AAU04552 standard; peptide; 9 AA.
 AC AAU04552;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 DE VEGF based bicyclic dimeric peptide #9.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
 XX diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 PH Disulfide-bond 1
 FT /note= "A disulfide bond forms between residue 1 and
 FT residue 17 of the sequence appearing as AAU04527, forming
 FT a dimeric peptide"
 FT Disulfide-bond 2..9
 FT /note= "This bond cyclises the peptide"
 FT
 XX WO200152875-A1.
 XX
 XX 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 XX
 PR 16-MAY-2000; 2000US-0204590P.
 PR

XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 DR
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX Example 26; Page 49; 102pp; English.
 PS
 XX The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX SQ Sequence 9 AA;

Query Match 90.9%; Score 50; DB 4; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCNEESLIC 9
 |||||
 Db 1 CCNEESLIC 9
 |||||
 RESULT 3
 AAU04553
 ID AAU04553 standard; peptide; 9 AA.
 XX
 XX AAU04553;
 AC
 XX 26-SEP-2001 (first entry)
 DT
 DE VEGF based bicyclic dimeric peptide #10.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
 XX diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 PH Disulfide-bond 1
 FT /note= "A disulfide bond forms between residue 1 and
 FT residue 17 of the sequence appearing as AAU04527, forming
 FT a dimeric peptide"
 FT Disulfide-bond 2..9
 FT /note= "This bond cyclises the peptide"
 FT
 XX WO200152875-A1.
 XX
 XX 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 XX
 PR 16-MAY-2000; 2000US-0204590P.
 PR

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FT residue 17 of the sequence appearing as AAU04527, forming
FT a dimeric peptide"
FT Disulfide-bond 2..9 /note= "This bond cyclises the peptide"
FT
XX WO200152875-A1.
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US001533.
XX
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stackler S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
XX Example 26; Page 49; 102pp; English.
XX
XX The sequence represents a dimeric bicyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGF (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX metha carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy
XX
XX Sequence 9 AA;
XX
XX Query Match 89.1%; Score 49; DB 4; Length 9;
XX Best Local Similarity 77.8%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCNEESLIC 9
XX 1 CCNEETVIC 9
XX
XX RESULT 4
XX AAU04525
XX ID AAU04525 standard; peptide; 8 AA.
XX
XX AC AAU04525;
XX
XX DT 26-SEP-2001 (first entry)

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XX VEGF based monocyclic peptide 2.
XX
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX diabetes induced neovascular sequelae; rheumatoid arthritis;
XX diabetic retinopathy; chronic inflammation; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 1..8 /note= "This bond cyclises the peptide"
XX
XX WO200152875-A1.
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US001533.
XX
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stackler S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
XX Claim 49; Page 32; 102pp; English.
XX
XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGF (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX metha carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy
XX
XX Sequence 8 AA;
XX
XX Query Match 83.6%; Score 46; DB 4; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 CNEESLIC 9
XX 1 CNEESLIC 8
XX
XX QY
XX DB

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RESULT 5
AAU04539 ID AAU04539 standard; peptide; 8 AA.
XX AC AAU04539;
XX DT 26-SEP-2001 (first entry)
XX DE VEGF based monocyclic peptide 17.
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX OS Synthetic.
XX Key Location/Qualifiers
FH Disulfide-bond 1..8
FT /note= "This bond cyclises the peptide"
XX WO200152875-A1.
XX 26-JUL-2001.
XX 18-JAN-2001; 2001WO-US001533.
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX Example 25; Page 47; 102pp; English.
XX The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGFD (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a
CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty stenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere
CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy

SQ Sequence 8 AA;
Query Match 78.2%; Score 43; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. NO. 1.4e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 CNEESLIC 9
DB 1 CNEETLIC 8
RESULT 6
AAU04541 ID AAU04541 standard; peptide; 8 AA.
XX AC AAU04541;
XX DT 26-SEP-2001 (first entry)
XX DE VEGF based monocyclic peptide 19.
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX OS Synthetic.
XX Key Location/Qualifiers
FH Disulfide-bond 1..8
FT /note= "This bond cyclises the peptide"
XX WO200152875-A1.
XX 26-JUL-2001.
XX 18-JAN-2001; 2001WO-US001533.
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX Example 25; Page 47; 102pp; English.
XX The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGFD (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a
CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty stenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability

CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 8 AA;

Query Match 76.4%; Score 42; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CNEESLIC 9
 DB 1 CNEESVVC 8
 |||||:|

RESULT 7
 AAU04538
 ID AAU04538 standard; peptide; 8 AA.
 XX
 AC AAU04538;
 DT 26-SEP-2001 (first entry)
 DE VEGF based monocyclic peptide 16.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"
 FT
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 PS Example 25; Page 47; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.

CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 8 AA;

Query Match 74.5%; Score 41; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CNEESLIC 9
 DB 1 CNEESLIC 8
 |||||:|

RESULT 8
 AAU04540
 ID AAU04540 standard; peptide; 8 AA.
 XX
 AC AAU04540;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 18.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"
 FT
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 PS Example 25; Page 47; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,

CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX SQ Sequence 8 AA;

Query Match 70.9%; Score 39; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CNEESLIC 9
 DB 1 CNEDSFIC 8
 |||:|

RESULT 9
 AAU08451
 ID AAU08451 standard; peptide; 8 AA.

XX AC AAU08451;
 XX DT 21-NOV-2001 (first entry)
 XX DE Peptide A6 encoded by human VEGF-A forward primer A6-F.
 XX KW Human; vascular endothelial growth factor; VEGF-A; vasculogenesis;
 KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
 KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;
 KW primer; mutant; mutein.

XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200162942-A2.
 XX PD 30-AUG-2001.

XX PF 26-FEB-2001; 2001WO-US006113.
 XX PR 25-FEB-2000; 2000US-0185205P.
 XX PR 18-MAY-2000; 2000US-0205331P.
 XX XX (LUDW-) LUDWIG INST CANCER RES.
 XX PA (LICN) LICENTIA OY.

XX PI Alitalo K, Jeltsch MM;
 XX DR WPI; 2001-536640/59.
 XX DR N-PSDB; AAS12807.

PT Polypeptides that bind cellular receptors for vascular endothelial growth
 PT factors, polynucleotides encoding them.

XX PS Claim 9; Fig 7C; 26lpp; English.

XX CC The present invention relates to polypeptides that bind cellular
 CC receptors for vascular endothelial growth factors (VEGFs), the
 CC polynucleotides encoding them, and their use for identifying agents that
 CC modulate interactions between VEGFs and their receptors. VEGFs and their
 CC receptors play an important role in vasculogenesis, the development of
 CC the embryonic vasculature from early differentiating endothelial cells
 CC and angiogenesis, the process of forming new blood vessels from pre-
 CC existing ones. Modulators of interactions between VEGF and its receptors
 CC may be used to treat dysfunction of the endothelial cell regulatory
 CC system. Such disorders include cancers, abnormal angiogenesis, rheumatoid
 CC proliferative retinopathies, age-related macular degeneration, rheumatoid
 CC arthritis and psoriasis. The polypeptides of the invention exhibit unique
 CC receptor binding profiles compared to known naturally occurring VEGFs.
 CC AAU08446-AAU08454 represent the peptides A1-A9 which are encoded by human
 CC VEGF-A forward primers used in the methods of the present invention

XX SQ Sequence 8 AA;

Query Match 63.6%; Score 35; DB 4; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCNEESL 7
 DB 2 CCNDEGL 8
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RESULT 10
 AAU08460
 ID AAU08460 standard; peptide; 8 AA.

XX AC AAU08460;
 XX DT 21-NOV-2001 (first entry)

XX DE Peptide C6 encoded by human VEGF-C forward primer C6-F.

XX KW Human; vascular endothelial growth factor; VEGF-C; vasculogenesis;
 KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
 KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;
 KW primer; mutant; mutein.

XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200162942-A2.
 XX PD 30-AUG-2001.

XX PF 26-FEB-2001; 2001WO-US006113.
 XX PR 25-FEB-2000; 2000US-0185205P.
 XX PR 18-MAY-2000; 2000US-0205331P.

XX XX (LUDW-) LUDWIG INST CANCER RES.
 XX PA (LICN) LICENTIA OY.

XX PI Alitalo K, Jeltsch MM;
 XX DR WPI; 2001-536640/59.
 XX DR N-PSDB; AAS12826.

XX PT Polypeptides that bind cellular receptors for vascular endothelial growth
 XX factors, polynucleotides encoding them.

XX PS Claim 9; Fig 7C; 26lpp; English.

XX CC The present invention relates to polypeptides that bind cellular

CC receptors for vascular endothelial growth factors (VEGFs), the
 CC polynucleotides encoding them, and their use for identifying agents that
 CC modulate interactions between VEGFs and their receptors. VEGFs and their
 CC receptors play an important role in vasculogenesis, the development of
 CC the embryonic vasculature from early differentiating endothelial cells
 CC and angiogenesis, the process of forming new blood vessels from pre-
 CC existing ones. Modulators of interactions between VEGF and its receptors
 CC may be used to treat dysfunction of the endothelial cell regulatory
 CC system. Such disorders include cancers, abnormal angiogenesis, rheumatoid
 CC proliferative retinopathies, age-related macular degeneration, arthritis
 CC and psoriasis. The polypeptides of the invention exhibit unique
 CC receptor binding profiles compared to known naturally occurring VEGFs.
 CC AAU08455-AAU08463 represent the peptides C1-C9 which are encoded by human
 CC VEGF-C forward primers used in the methods of the present invention
 XX
 SQ Sequence 8 AA;

Query Match 60.0%; Score 33; DB 4; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEESL 7
 |||||
 DB 2 CCNSEGL 8

RESULT 11
 ABR29819
 ID ABR29819 standard; peptide; 9 AA.

XX AC ABR29819;
 XX DT 19-MAY-2003 (first entry)
 XX DE Human cancer-related protein 192P2G7 HLA peptide #1263.
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 XX human leukocyte antigen.
 XX OS Homo sapiens.
 XX PN WO200283921-A2.
 XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.
 XX PR 10-APR-2001; 2001US-0282739P.
 XX PR 10-APR-2001; 2001US-0283112P.
 XX PR 25-APR-2001; 2001US-0286630P.
 XX PA (AGEN-) AGENSYS INC.
 XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.

XX DR New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX PS Claim 13; Page 431; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 9 AA;

Query Match 60.0%; Score 33; DB 6; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCNEESL 7
 |||||
 DB 1 CCNAEAL 7

RESULT 12
 ABR28797
 ID ABR28797 standard; peptide; 9 AA.

XX AC ABR28797;
 XX DT 19-MAY-2003 (first entry)
 XX DE Human cancer-related protein 192P2G7 HLA peptide #241.
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 XX human leukocyte antigen.
 XX OS Homo sapiens.
 XX PN WO200283921-A2.
 XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.
 XX PR 10-APR-2001; 2001US-0282739P.
 XX PR 10-APR-2001; 2001US-0283112P.
 XX PR 25-APR-2001; 2001US-0286630P.
 XX PA (AGEN-) AGENSYS INC.
 XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.

XX DR New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX PS Claim 13; Page 419; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX SQ Sequence 9 AA;

Query Match 60.0%; Score 33; DB 6; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 CCNEESL 7
Db      1 CCNAEAL 7

RESULT 13
ID ABR29456 standard; peptide; 9 AA.
XX
AC ABR29456;
XX
XX 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 192P2G7 HLA peptide #900.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 427; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
Query Match 60.0%; Score 33; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCNEESL 7
Db      1 CCNAEAL 7

RESULT 14
ID ABR28814 standard; peptide; 9 AA.
XX
AC ABR28814;
XX
XX 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 192P2G7 HLA peptide #258.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 419; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
Query Match 60.0%; Score 33; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCNEESL 7
Db      1 CCNAEAL 7

RESULT 15
ID ABR29789 standard; peptide; 9 AA.
XX
AC ABR29789;
XX
XX 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 192P2G7 HLA peptide #1233.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.

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XX WO200283921-A2.
XX
XX
PD 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 431; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX
XX Sequence 9 AA;
SQ
Query Match 60.0%; Score 33; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db 3 CCNAEAL 9

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-761-636A-9
Perfect score: 55
Sequence: 1 CCNEESLIC 9

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Gapop 10.0 , Gapext 0.5

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Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	50	90.9	9	9	US-09-761-636A-33	Sequence 33, Appl
3	49	89.1	9	9	US-09-761-636A-34	Sequence 34, Appl
4	46	83.6	8	9	US-09-761-636A-6	Sequence 6, Appli
5	43	78.2	8	9	US-09-761-636A-20	Sequence 20, Appl
6	42	76.4	8	9	US-09-761-636A-22	Sequence 22, Appl
7	41	74.5	8	9	US-09-761-636A-19	Sequence 19, Appl
8	39	70.9	8	9	US-09-761-636A-21	Sequence 21, Appl
9	35	63.6	8	9	US-09-795-006A-133	Sequence 133, App
10	33	60.0	8	9	US-09-795-006A-142	Sequence 142, App
11	29	52.7	5	12	US-10-436-549-605	Sequence 605, App
12	27	49.1	9	14	US-10-072-602B-292	Sequence 292, App
13	26	47.3	8	10	US-09-984-271-199	Sequence 199, App
14	26	47.3	8	12	US-09-984-276-199	Sequence 199, App
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16	26	47.3	8	15	US-10-149-138-2515	Sequence 2515, Ap
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20	26	47.3	9	14	US-10-264-374-93	Sequence 93, Appl
21	26	47.3	9	14	US-10-375-992-93	Sequence 93, Appl
22	26	47.3	9	14	US-10-286-457-109	Sequence 109, App
23	26	47.3	9	15	US-10-149-138-2516	Sequence 2516, Ap
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25	26	47.3	9	15	US-10-149-138-4029	Sequence 4029, Ap
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27	26	47.3	9	16	US-10-264-374-93	Sequence 93, Appl
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29	26	47.3	9	16	US-10-149-138-3064	Sequence 3064, Ap
30	26	47.3	9	16	US-10-149-138-4029	Sequence 4029, Ap
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34	25	45.5	8	14	US-10-012-806A-13	Sequence 13, Appl
35	25	45.5	8	14	US-10-012-806A-15	Sequence 15, Appl
36	25	45.5	8	14	US-10-012-806A-19	Sequence 19, Appl
37	25	45.5	8	14	US-10-012-806A-37	Sequence 37, Appl
38	25	45.5	9	10	US-09-942-052-46	Sequence 46, Appl
39	25	45.5	9	10	US-09-942-052-126	Sequence 126, App
40	25	45.5	9	10	US-09-942-052-216	Sequence 216, App
41	25	45.5	9	14	US-10-072-602B-509	Sequence 509, App
42	25	45.5	9	14	US-10-012-806A-11	Sequence 11, Appl
43	25	45.5	9	14	US-10-286-457-354	Sequence 354, App
44	24	43.6	8	9	US-09-826-290-367	Sequence 367, App
45	24	43.6	8	14	US-10-006-869-917	Sequence 917, App

ALIGNMENTS

RESULT 1
US-09-761-636A-9
; Sequence 9, Application US/09761636A
; Patent No. US20020085218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-9

Query Match 100.0%; Score 55; DB 9; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9
Db 1 CCNEESLIC 9

RESULT 2
US-09-761-636A-33
; Sequence 33, Application US/09761636A
; Patent No. US20020085218A1

GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-33

Query Match 90.9%; Score 50; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 9
Db 1 CNEESLIC 9

RESULT 3
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; Sequence 34, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-34

Query Match 89.1%; Score 49; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 9
Db 1 CNEETVIC 9

RESULT 4
US-09-761-636A-6
; Sequence 6, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6

Query Match 83.6%; Score 46; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CNEESLIC 9
Db 1 CNEESLIC 8

RESULT 5
US-09-761-636A-20
; Sequence 20, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-20

Query Match 78.2%; Score 43; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 CNEESLIC 9
Db 1 CNEETLIC 8

RESULT 6
US-09-761-636A-22
; Sequence 22, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293


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; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-22

Query Match          76.4%; Score 42; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CNEESLIC 9
Db 1 CNEESWVC 8

RESULT 7
US-09-761-636A-19
; Sequence 19, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-19

Query Match          74.5%; Score 41; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CNEESLIC 9
Db 1 CNEESLIC 8

RESULT 8
US-09-761-636A-21
; Sequence 21, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 21
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-21
```

```
Query Match          70.9%; Score 39; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 2 CNEESLIC 9
Db 1 CNEESDFIC 8
```

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RESULT 9
US-09-795-006A-133
; Sequence 133, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alicalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-006A-133
```

```
Query Match          63.6%; Score 35; DB 9; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CCNEESL 7
Db 2 CCNDEGL 8
```

```
RESULT 10
US-09-795-006A-142
; Sequence 142, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alicalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
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OTHER INFORMATION: peptide
US-09-795-006A-142

Query Match 60.0%; Score 33; DB 9; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNERSL 7
|||
DB 2 CCNSEGL 8
|||

RESULT 11

US-10-436-549-605

Sequence 605, Application US/10436549
Publication No. US20040038307A1

GENERAL INFORMATION:

APPLICANT: Meng, Frank D.

APPLICANT: Chan, John W.

APPLICANT: Zhang, Shengsheng

APPLICANT: Benkovic, Stephen J.

TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN

TITLE OF INVENTION: PROTEIN ANALYSIS

FILE REFERENCE: ENG8-P01-001

CURRENT APPLICATION NUMBER: US/10/436,549

CURRENT FILING DATE: 2003-05-12

PRIOR APPLICATION NUMBER: 60/379,626

PRIOR FILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: 60/393,233

PRIOR FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: 60/393,235

PRIOR FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: 60/393,211

PRIOR FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: 60/393,280

PRIOR FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: 60/393,197

PRIOR FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: 60/393,223

PRIOR FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: 60/430,948

PRIOR FILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: 60/433,319

PRIOR FILING DATE: 2002-12-13

PRIOR APPLICATION NUMBER: 60/393,137

PRIOR FILING DATE: 2002-07-01

NUMBER OF SEQ ID NOS: 614

SOFTWARE: PatentIn version 3.2

SEQ ID NO 605

LENGTH: 5

TYPE: PRT

ORGANISM: human

US-10-436-549-605

Query Match 52.7%; Score 29; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNE 4
|||
DB 2 CCNE 5
|||

RESULT 12

US-10-072-602B-292

Sequence 292, Application US/10072602B

Publication No. US20030109670A1

GENERAL INFORMATION:

APPLICANT: University of Utah Research Foundation

APPLICANT: Cognetix, Inc.

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J, Michael

APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 292
LENGTH: 9
TYPE: PRT
ORGANISM: Conus dalli
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(9)
OTHER INFORMATION: Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is Tyr,
OTHER INFORMATION: Trp (D or L) or bromo-Trp (D or L); Xaa at residue 4 is Tyr,
OTHER INFORMATION: 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
OTHER INFORMATION: O-phospho-Tyr
US-10-072-602B-292

Query Match 49.1%; Score 27; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCNERSLIC 9
|||
DB 1 CCXXXKLC 9
|||

RESULT 13

US-09-984-271-199

Sequence 199, Application US/09984271

Publication No. US20030040088A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 71 Human Secreted Proteins

FILE REFERENCE: PZ030PI

CURRENT APPLICATION NUMBER: US/09/984,271

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: 09/482,273

PRIOR FILING DATE: 2000-01-13

PRIOR APPLICATION NUMBER: PCT/US99/15849

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: 60/092,921

PRIOR FILING DATE: 1998-07-15

PRIOR APPLICATION NUMBER: 60/092,922

PRIOR FILING DATE: 1998-07-15

PRIOR APPLICATION NUMBER: 60/092,956

PRIOR FILING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 267

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 199

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

US-09-984-271-199

Query Match 47.3%; Score 26; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNE 4
|||
DB 1 CCNQ 4
|||

RESULT 14

US-09-984-276-199
; Sequence 199, Application US/09984276
; Publication No. US20030017500A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/984,276
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-276-199

Query Match 47.3%; Score 26; DB 12; Length 8;
Best Local Similarity 75.0%; Pred.No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNE 4
DB 1 CCNQ 4

RESULT 15

US-10-149-138-2497
; Sequence 2497, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2497
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2497

Query Match 47.3%; Score 26; DB 15; Length 8;
Best Local Similarity 60.0%; Pred.No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNEE 5

Db 1 CCHEQ 5

Search completed: September 5, 2004, 11:15:59
Job time : 36.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:01:38 ; Search time 12 seconds

(without alignments)
38,719 Million cell updates/sec

Title: US-09-761-636A-9

Perfect score: 55

Sequence: 1 CNEESLIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	54.5	8	3	US-09-100-409A-27
2	27	49.1	8	5	PCT-US93-05325-2
3	27	49.1	8	5	PCT-US93-05325-30
4	27	49.1	8	5	PCT-US93-05325-31
5	27	49.1	8	5	PCT-US93-05325-32
6	26	47.3	8	4	US-09-089-878-3
7	26	47.3	8	4	US-09-482-273-199
8	26	47.3	9	3	US-09-258-754-13
9	26	47.3	9	3	US-09-139-802-93
10	26	47.3	9	3	US-09-042-107-13
11	26	47.3	9	4	US-09-659-786-93
12	26	47.3	9	4	US-08-926-914-93
13	26	47.3	9	4	US-09-722-250D-13
14	25	45.5	8	1	US-08-107-411-7
15	25	45.5	8	1	US-08-397-633A-100
16	25	45.5	8	3	US-09-258-754-49
17	25	45.5	8	3	US-09-042-107-49
18	25	45.5	8	4	US-09-722-250D-49
19	25	45.5	9	4	US-09-535-852-1205
20	24	43.6	4	3	US-08-750-142B-17
21	24	43.6	5	4	US-09-708-606-22
22	24	43.6	6	4	US-09-708-606-8
23	24	43.6	6	4	US-09-708-606-26
24	24	43.6	7	3	US-08-750-142B-37
25	24	43.6	7	4	US-09-717-364A-32
26	24	43.6	7	4	US-09-708-606-11
27	24	43.6	8	4	US-09-187-859-917

28	24	43.6	8	4	US-09-839-542B-917	Sequence 917, Appl
29	24	43.6	8	4	US-09-708-606-20	Sequence 20, Appl
30	24	43.6	9	4	US-09-535-852-927	Sequence 927, Appl
31	24	43.6	9	4	US-09-708-606-10	Sequence 10, Appl
32	23	41.8	7	3	US-08-973-551-14	Sequence 14, Appl
33	23	41.8	8	2	US-08-520-535-3	Sequence 3, Appl
34	23	41.8	8	2	US-09-079-432-3	Sequence 3, Appl
35	23	41.8	8	3	US-09-258-754-33	Sequence 33, Appl
36	23	41.8	8	3	US-09-258-754-42	Sequence 42, Appl
37	23	41.8	8	3	US-09-258-754-214	Sequence 214, Appl
38	23	41.8	8	3	US-09-042-107-33	Sequence 33, Appl
39	23	41.8	8	3	US-09-042-107-42	Sequence 42, Appl
40	23	41.8	8	3	US-09-042-107-214	Sequence 214, Appl
41	23	41.8	8	3	US-08-160-604-79	Sequence 79, Appl
42	23	41.8	8	3	US-08-160-604-80	Sequence 80, Appl
43	23	41.8	8	4	US-09-314-268-61	Sequence 61, Appl
44	23	41.8	8	4	US-09-314-268-62	Sequence 62, Appl
45	23	41.8	8	4	US-09-314-268-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1

US-09-100-409A-27
; Sequence 27, Application US/09100409A
; Patent No. 6090388
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND
; TITLE OF INVENTION: IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,409A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-100-409A-27

Query Match 54.5%; Score 30; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CNEESLIC 9

DB 1 CNOGSFLC 8

RESULT 2
PCT-US93-05325-2
; Sequence 2, Application PC/TUS9305325
; GENERAL INFORMATION:
; APPLICANT: SRI, INTERNATIONAL
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
; TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
; ADDRESSEE: COUNSEL
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05325
; FILING DATE: 19930603
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,497
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: PCT-2679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-2446
; TELEFAX: (415) 859-3880
; TELEX: 334486
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is modified
; OTHER INFORMATION: with Acn."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is modified
; OTHER INFORMATION: with Acn."
; PCT-US93-05325-2

Query Match 49.1%; Score 27; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6
Db 3 CCNTSS 8

RESULT 3
PCT-US93-05325-30
; Sequence 30, Application PC/TUS9305325
; GENERAL INFORMATION:
; APPLICANT: SRI, INTERNATIONAL
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
; TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
; ADDRESSEE: COUNSEL
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05325
; FILING DATE: 19930603
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,497
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05325
; FILING DATE: 19930603
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,497
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: PCT-2679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-2446
; TELEFAX: (415) 859-3880
; TELEX: 334486
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is modified
; OTHER INFORMATION: with Acn."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is modified
; OTHER INFORMATION: with Acn."
; PCT-US93-05325-30

Query Match 49.1%; Score 27; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6
Db 3 CCNTSS 8

RESULT 4
PCT-US93-05325-31
; Sequence 31, Application PC/TUS9305325
; GENERAL INFORMATION:
; APPLICANT: SRI, INTERNATIONAL
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
; TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
; ADDRESSEE: COUNSEL
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05325
; FILING DATE: 19930603
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,497
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.
 REGISTRATION NUMBER: 34,799
 REFERENCE/DOCKET NUMBER: PCT-2679
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 859-2446
 TELEFAX: (415) 859-3880
 TELEX: 334486
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: Both
 MOLECULE TYPE: peptide
 PCT-US93-05325-31

Query Match 49.1%; Score 27; DB 5; Length 8;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6
 |||||
 Db 3 CCNTSS 8

RESULT 5

PCT-US93-05325-32
 Sequence 32, Application PC/TUS9305325
 GENERAL INFORMATION:

APPLICANT: SRI, INTERNATIONAL
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
 TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
 ADDRESSEE: COUNSEL
 STREET: 333 Ravenswood Avenue
 CITY: Menlo Park
 STATE: California
 COUNTRY: USA
 ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/05325
 FILING DATE: 19930603

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/894,497
 FILING DATE: 05-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.
 REGISTRATION NUMBER: 34,799
 REFERENCE/DOCKET NUMBER: PCT-2679
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 859-2446
 TELEFAX: (415) 859-3880
 TELEX: 334486

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 3..4

OTHER INFORMATION: /note= "This position has disulfide

OTHER INFORMATION: bond to corresponding position of identical

OTHER INFORMATION: sequence."

PCT-US93-05325-32

Query Match 49.1%; Score 27; DB 5; Length 8;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6
 |||||
 Db 3 CCNTSS 8

RESULT 6

US-09-089-878-3
 Sequence 3, Application US/09089878
 Patent No. 6458528

GENERAL INFORMATION:
 APPLICANT: Groat, Randall G.
 APPLICANT: O'Connor, Thomas P.
 APPLICANT: Mermer, Brian
 TITLE OF INVENTION: DIAGNOSIS OF FELINE IMMUNODEFICIENCY VIRUS INFECTION
 TITLE OF INVENTION: USING ENV/GAG POLYPEPTIDE MARKERS
 FILE REFERENCE: 00088/111001

CURRENT APPLICATION NUMBER: US/09/089,878
 CURRENT FILING DATE: 1998-06-03
 EARLIER APPLICATION NUMBER: US 60/085,615
 EARLIER FILING DATE: 1998-05-15
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 3

LENGTH: 8

TYPE: PRT

ORGANISM: feline immunodeficiency virus

US-09-089-878-3

Query Match 47.3%; Score 26; DB 4; Length 8;
 Best Local Similarity 37.5%; Pred. No. 3e+05;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CNEESLIC 9
 |||||
 Db 1 CNQNOFFC 8

RESULT 7

US-09-482-273-199
 Sequence 199, Application US/09482273
 Patent No. 6534631

GENERAL INFORMATION:

APPLICANT: Rosen et al.
 TITLE OF INVENTION: 71 Human Secreted Proteins
 FILE REFERENCE: P2030P1
 CURRENT APPLICATION NUMBER: US/09/482,273
 CURRENT FILING DATE: 2000-01-13
 EARLIER APPLICATION NUMBER: PCT/US99/15849
 EARLIER FILING DATE: 1999-07-14
 EARLIER APPLICATION NUMBER: 60/092,921
 EARLIER FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: 60/092,922
 EARLIER FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: 60/092,956
 EARLIER FILING DATE: 1998-07-15
 NUMBER OF SEQ ID NOS: 267
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 199

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

US-09-482-273-199

Query Match 47.3%; Score 26; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 3e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNE 4

Db 1 CCNQ 4

RESULT 8

US-09-258-754-13
; Sequence 13, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-13

Query Match 47.3%; Score 26; DB 3; Length 9;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9

Db 1 CLAKENVVC 9

RESULT 9

US-09-139-802-93
; Sequence 93, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-139-802-93

Query Match 47.3%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9

Db 1 CPEHRSIVC 9

RESULT 10

US-09-042-107-13
; Sequence 13, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-13

Query Match 47.3%; Score 26; DB 3; Length 9;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9

Db 1 CLAKENVVC 9

RESULT 11

US-09-659-786-93
; Sequence 93, Application US/09659786
; Patent No. 6491894
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/659,786
; CURRENT FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-659-786-93

Query Match 47.3%; Score 26; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9

Db 1 CPEHRSIVC 9

RESULT 12

US-08-926-914-93
; Sequence 93, Application US/08926914

Patent No. 6576239
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-926-914-93

Query Match 47.3%; Score 26; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9
Db 1 CPEHRSLVC 9

RESULT 13
US-09-722-250D-13
; Sequence 13, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-13

Query Match 47.3%; Score 26; DB 4; Length 9;
Best Local Similarity 33.3%; Pred. No. 3e+05;

Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCNEESLIC 9
Db 1 CLAKENVVC 9
RESULT 14
US-08-107-411-7
; Sequence 7, Application US/08107411
; Patent No. 5340726
; GENERAL INFORMATION:
; APPLICANT: Waxman, Lloyd
; APPLICANT: Connolly, Thomas M.
; APPLICANT: Keller, Paul
; TITLE OF INVENTION: PROTEIN FOR INHIBITING
; TITLE OF INVENTION: COLLAGEN-STIMULATED PLATELET AGGREGATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: N.J.
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/844,303
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farr, Richard S.
; REGISTRATION NUMBER: 32,586
; REFERENCE/DOCKET NUMBER: 18415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4958
; TELEFAX: (908) 594-4720
; TELEX: () 138825
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-107-411-7

Query Match 45.5%; Score 25; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNEE 5
Db 4 CCDEK 8

RESULT 15
US-08-397-633A-100
; Sequence 100, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:

Sun Sep 5 11:41:21 2004

ADDRESSES: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/HIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-633A-100

Query Match 45.5%; Score 25; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 CNEESLIC 9
Db 1 CGOSKVIC 8

Search completed: September 5, 2004, 11:07:04
Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:00:28 ; Search time 11.6667 Seconds
(without alignments)
74.205 Million cell updates/sec

Title: US-09-761-636A-10
Perfect score: 50
Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	34.0	8	2 G33098	205K exoantigen -
2	16	32.0	9	2 A60356	118K stomach cancer
3	16	32.0	9	2 PT0247	Ig heavy chain CRD
4	15	30.0	5	2 A60521	glycogen phosphory
5	15	30.0	6	2 I65546	MHC H2-L antigen -
6	15	30.0	7	2 PH0932	T-cell receptor be
7	15	30.0	8	2 PH0803	T-cell receptor al
8	14	28.0	5	2 E60274	major protein anti
9	14	28.0	6	2 F41946	T-cell receptor ga
10	14	28.0	8	2 A42057	fibroblast growth
11	14	28.0	8	2 A35180	neutral proteinase
12	14	28.0	9	2 A60522	sperm-activating p
13	14	28.0	9	2 B41983	orf downstream to b
14	14	28.0	9	2 I52974	seminal vesicle pr
15	13	26.0	6	2 I49421	laminin B1 - weste
16	13	26.0	6	2 S29881	Na+/K+-exchanging
17	13	26.0	7	2 A12016	formylglycinamide
18	13	26.0	7	2 S42620	aggrekan - bovine
19	13	26.0	8	2 S59622	metallothionein is
20	13	26.0	8	2 PQ0701	unidentified 6.5/3
21	13	26.0	9	2 PT0268	Ig heavy chain CRD
22	12	24.0	6	4 A35039	hypothetical colla
23	12	24.0	7	2 E61491	seed protein ws-5
24	12	24.0	8	2 S71919	alcohol dehydrogen
25	12	24.0	8	2 S10783	enamelin f - bovin
26	12	24.0	9	2 S3636	coat protein beta
27	12	24.0	9	2 G58502	kidney and bladder
28	12	24.0	9	2 S70334	endosperm protein,
29	11	22.0	4	2 A32039	tyrosine-melanocyt

30 11 22.0 4 2 I54357 schwannomin - mous
31 11 22.0 5 2 B22565 R-phycoerythrin al
32 11 22.0 6 2 B34835 dnaA protein - pse
33 11 22.0 6 2 PT0280 Ig heavy chain CRD
34 11 22.0 7 2 ECMUCR catch-relaxing pep
35 11 22.0 7 2 I48105 dihydrofolate redu
36 11 22.0 7 2 I48086 DNA topoisomerase
37 11 22.0 7 2 PH1602 Ig H chain V-D-J r
38 11 22.0 8 2 S19288 acylase - Kluyvera
39 11 22.0 8 2 B39745 endoglycosylcerami
40 11 22.0 8 2 S68802 nitrate reductase
41 11 22.0 8 2 S21288 lectin - potato (f
42 11 22.0 8 2 PT0530 T-cell receptor be
43 11 22.0 8 2 I57018 gene Ctrr protein
44 11 22.0 8 2 A42689 major postsynaptic
45 11 22.0 8 4 I54017 granulocyte-colony

ALIGNMENTS

RESULT 1
G33098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: G33098
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: G33098
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-8 <NIC>

Query Match 34.0%; Score 17; DB 2; Length 8;
Best Local Similarity 66.7%; Pred No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSV 8
DB 2 VPLXLV 7

RESULT 2
A60356
118K stomach cancer antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C:Accession: A60356
R:Shiraishi, Y.
Int. J. Cancer 45, 783-787, 1990
A:Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A:Reference number: A60356; MUID:90216080; PMID:2323853
A:Accession: A60356
A:Molecule type: protein
A:Residues: 1-9 <SHI>
C:Keywords: glycoprotein

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSV 8
DB 1 IPLKPV 6

RESULT 3
PT0247
Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0247
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0247
 A;Molecule type: DNA
 A;Residues: 1-9 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 32.0%; Score 16; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SVPLTS 7
 |||
 Db 2 SAPIDS 7

RESULT 4
 A60521
 glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
 N;Alternate names: glycogen phosphorylase b
 C;Species: Liza ramada
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
 C;Accession: A60521
 R;Bonamusa, L.; Baanante, I.V.
 Comp. Biochem. Physiol. B 95, 295-301, 1990

A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
 A;Reference number: A60521; MUID:90227907; PMID:2109669
 A;Accession: A60521
 A;Molecule type: protein
 A;Residues: 1-5 <BON>

C;Superfamily: glucan phosphorylase
 C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
 F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match 30.0%; Score 15; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
 |||
 Db 3 SVP 5

RESULT 5
 I65546
 MHC H2-L antigen - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C;Accession: I65546
 R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
 Cell 44, 261-272, 1986
 A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and the
 A;Reference number: I52778; MUID:96106202; PMID:3510743
 A;Accession: I65546
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>
 A;Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234

Query Match 30.0%; Score 15; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPILT 6
 |||
 Db 2 VPCT 5

RESULT 6

PH0932
 T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0932
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
 A;Reference number: PH0891; MUID:92078857; PMID:1836012
 A;Accession: PH0932
 A;Molecule type: mRNA
 A;Residues: 1-7 <GOL>
 A;Experimental source: complete Freund's adjuvant-immunized lymph node
 C;Keywords: T-cell receptor

Query Match 30.0%; Score 15; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLT 4
 |||
 Db 1 CASP 4

RESULT 7
 PH0803
 T-cell receptor alpha chain (J2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PH0803
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r
 allelic exclusion and antigen-specific repertoire.
 A;Reference number: PH0746; MUID:92078846; PMID:1836010
 A;Accession: PH0803
 A;Molecule type: mRNA
 A;Residues: 1-8 <CAS>
 A;Cross-references: EMBL:X60912
 A;Experimental source: T lymphocyte
 C;Keywords: T-cell receptor

Query Match 30.0%; Score 15; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLT 6
 |||
 Db 1 CAAGIT 6

RESULT 8
 E60274
 major protein antigen MP763 - Mycobacterium tuberculosis (fragment)
 C;Species: Mycobacterium tuberculosis
 C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C;Accession: E60274
 R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A;Title: Isolation and partial characterization of major protein antigens in the culture
 A;Reference number: A60274; MUID:91099989; PMID:1898899
 A;Accession: E60274
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <NAG>

Query Match 28.0%; Score 14; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLT 6
 |||
 Db 3 PIT 5

RESULT 9
F41946
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: F41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: F41946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <WHE>
C:Keywords: T-cell receptor

Query Match 28.0%; Score 14; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSV 3
DB 2 CAV 4

RESULT 10
A42057
fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42057
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A:Title: Differential splicing in the extracellular region of fibroblast growth factor
A:Reference number: A42057; MUID:92107200; PMID:1309595
A:Accession: A42057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <WER>
A:Cross-references: GB:M80363
C:Keywords: growth factor receptor

Query Match 28.0%; Score 14; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPLTS 7
DB 1 VLLTS 5

RESULT 11
A35180
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C:Accession: A35180
R:Oshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
J. Biol. Chem. 265, 5809-5815, 1990
A:Title: Purification of a novel type of calcium-activated neutral protease from rat brain
A:Reference number: A35180; MUID:90202830; PMID:2319836
A:Accession: A35180
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <YOS>
C:Keywords: hydrolase

Query Match 28.0%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTS 7
DB 1 PLLS 4

RESULT 12
A60522
sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)
C:Species: Diadema setosum
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: A60522
R:Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzuki
Comp. Biochem. Physiol. B 95, 423-429, 1990
A:Title: A species-specific sperm-activating peptide from the egg jelly of the sea urchin
A:Reference number: A60522; MUID:90227916; PMID:2158412
A:Accession: A60522
A:Molecule type: protein
A:Residues: 1-9 <YOS>
C:Superfamily: unassigned animal peptides
F:2-9/Disulfide bonds: #status experimental

Query Match 28.0%; Score 14; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 SVC 9
DB 7 AVC 9

RESULT 13
B41983
orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)
C:Species: Azotobacter vinelandii
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: B41983
R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
A:Title: Unification of the ferritin family of proteins.
A:Reference number: A41983; MUID:92196129; PMID:1549605
A:Accession: B41983
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-9 <GRO>
A:Cross-references: GB:M83692; NID:gl42297; PIDN:AAA22122.1; PID:gl42299
A:Note: sequence extracted from NCHI backbone (NCBIP:88442)

Query Match 28.0%; Score 14; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTS 7
DB 4 PRTS 7

RESULT 14
I52974
seminal vesicle protein IV - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I52974
R:Yang, C.T.; Harris, S.E.
DNA 2, 105-111, 1983
A:Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sites
A:Reference number: I52974; MUID:83261204; PMID:6307619
A:Accession: I52974
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <RES>
A:Cross-references: GB:M27324; NID:g207124; PIDN:AAA63501.1; PID:g207125
C:Genetics: SVSIV

Query Match 28.0%; Score 14; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTSV 8
| | | |
Db 3 LTSV 6

RESULT 15

I49421
laminin B1 - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49421
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I49334; MUID:94319082; PMID:8043949
A:Accession: I49421
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829

Query Match 26.0%; Score 13; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SVC 9
| | |
Db 3 SVC 5

Search completed: September 5, 2004, 11:06:22
Job time : 11.6667 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:57:02 ; Search time 7 Seconds
(without alignments)
66.947 Million cell updates/sec

Title: US-09-761-636A-10
Perfect score: 50
Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	19	38.0	9	1 MGMT_BOVIN	P29177 bos taurus
2	14	28.0	8	1 ACT_CARMA	P80709 carcinus ma
3	14	28.0	9	1 YBFR_AZOVI	P25825 azotobacter
4	13	26.0	6	1 EI01_LITRU	P82096 litorea rub
5	12	24.0	8	1 ALI6_CYPDO	P82157 cydia pomon
6	12	24.0	8	1 FUSF_FUSDO	P81010 fusarium so
7	12	24.0	8	1 UPAL_HUMAN	P30087 homo sapien
8	12	24.0	9	1 FAR5_PENMO	P83320 penaeus mon
9	12	24.0	9	1 FLA2_TREHY	P80159 treponema h
10	12	24.0	9	1 OXYA_SCYCA	P42996 scyliorhinu
11	12	24.0	9	1 OXYF_SCYCA	P42997 scyliorhinu
12	12	24.0	9	1 OXYT_BUFRE	P42995 bufo regula
13	12	24.0	9	1 OXYV_SQUAC	P43000 squalus aca
14	11	22.0	6	1 VP19_HSVIK	P23210 herpes simp
15	11	22.0	7	1 CARP_MYTED	P10420 mytilus edu
16	11	22.0	7	1 MNP1_LEPDE	P42984 leptinotars
17	11	22.0	7	1 TPYV_PACDA	P83455 pachymedusa
18	11	22.0	8	1 PPK3_PERAM	P84618 periplaneta
19	11	22.0	8	1 VGGH_HSV2B	P81780 herpes simp
20	11	22.0	9	1 COXE_THUOB	P80975 thunnus obe
21	11	22.0	9	1 FAR9_ASCSU	P43172 ascaris suu
22	11	22.0	9	1 ISOT_CYPCA	P42993 cyprinus ca
23	11	22.0	9	1 LMT3_LOCMI	P41489 locusta mig
24	11	22.0	9	1 OXYA_SQUAC	P42999 squalus aca
25	11	22.0	9	1 OXYT_EISFO	P42998 eisenia foe
26	11	22.0	9	1 OXYT_OCTVU	P80027 octopus vul
27	11	22.0	9	1 OXYT_RABIT	P32878 oryctolagus
28	11	22.0	9	1 RT33_BOVIN	P82926 bos taurus
29	11	22.0	9	1 TAL3_PICJA	P17441 pichia jadi
30	11	22.0	9	1 UPAA3_HUMAN	P30089 homo sapien
31	11	22.0	9	1 UPAA7_HUMAN	P30093 homo sapien
32	10	20.0	7	1 TY51_LITRU	P82065 litorea rub
33	10	20.0	8	1 UPAA_HUMAN	P30096 homo sapien

34 10 20.0 9 1 CCAP_CARMA P38556 carcinus ma
35 10 20.0 9 1 CONO_CONGE P05486 conus geogr
36 10 20.0 9 1 CONO_CONST P05487 conus stria
37 10 20.0 9 1 DNFI_LOCMI P16339 locusta mig
38 10 20.0 9 1 OXYT_CYPCA P23879 cyprinus ca
39 10 20.0 9 1 OXYT_RAJCL P42994 raja clavav
40 10 20.0 9 1 PPK1_PERAM P82691 periplaneta
41 10 20.0 9 1 TAL1_PICJA P17440 pichia jadi
42 9 18.0 5 1 EI03_LITRU P82099 litorea rub
43 9 18.0 6 1 CIP1_MYTED P13736 mytilus edu
44 9 18.0 6 1 CIP2_MYTED P13737 mytilus edu
45 9 18.0 7 1 BRHP_CONIM P58803 conus imper

ALIGNMENTS

RESULT 1
MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (Fragment).
DE methylguanine-DNA methyltransferase (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karan P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro: IPR001497; Methyltransf_1.
DR PROSITE: PS00374; MGMT; PARTIAL.
KW DNA repair; transferase; Methyltransferase.
FT NON_TER 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 38.0%; Score 19; DB 1; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+05;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 VPLTSVC 9
Db 3 IPILTPC 9

RESULT 2
ACT_CARMA STANDARD; PRT; 8 AA.
ID_ACT_CARMA
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Actin (Fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Rubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32(1996).
CC -1- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 kDa.
CC -1- SIMILARITY: Belongs to the actin family.
CC InterPro; IPR004001; Actin.
CC InterPro; IPR004000; Actin-like.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;
Query Match 28.0%; Score 14; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSVPVL 5
DB 2 CDVDI 6
RESULT 3
YBFR_AZOVI
ID YBFR_AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
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CC or send an email to license@isb-sib.ch).

CC EMBL; M83692; RAA22122.1; .
DR DR PIR; B41983; B41983.
KW Hypothetical protein.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;
Query Match 28.0%; Score 14; DB 1; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 PLTS 7
DB 4 PRTS 7
RESULT 4
EI01_LITRU
ID EI01_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 6
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 792 MW; 5683704772C9A000 CRC64;
Query Match 26.0%; Score 13; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 VPL 5
DB 2 VPI 4
RESULT 5
ALL6_CYPDPO
ID ALL6_CYPDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;
Query Match 24.0%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPL 5
Db 1 LPL 3

RESULT 6

FUSS FUSSO
ID_FUSS_FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s 13596* (Fragment)
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
[1]
RN SEQUENCE.
RP STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J.; Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -!- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON TER 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 24.0%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
Db 6 NVP 8

RESULT 7

UPAL HUMAN
ID_UPAL_HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE.
RP SEQUENCE.
RC TISSUE=Plasma;
RA MEDLINE=93092937; PubMed=1459097;
RX Hughes G.J.; Frutiger S.; Paquet N.; Ravier F.; Pasquali C.;
RA Sanchez J.-C.; James R.; Tissot J.-D.; Bjellqvist B.;
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 4.9, its MW is: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON TER 1
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 24.0%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
Db 5 NVP 7

RESULT 8

FARS_PENMO
ID_FARS_PENMO STANDARD; PRT; 9 AA.
AC P83320;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLPS (SMPSRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Eyestalk;
RC MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P.; Pupum J.; Krungkasem C.; Longyant S.;
RA Chaivuthangkura P.; Sithigorngul W.; Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.
DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
Db 1 SMP 3

RESULT 9

FLA2 TREHY
ID_FLA2_TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaA2 (35 kDa sheath protein) (Fragment).
GN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
[1]
RN SEQUENCE.
RP SEQUENCE.
RC STRAIN=CS;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H.; Baats E.; van Vorstenbosch C.J.A.H.V.;
RA van der Zeijst B.A.M.; Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are composed of two sheath proteins and three core proteins."
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -!- FUNCTION: Component of the outer layer of the flagella.
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE THAT CONTAINS THREE PROTEINS FLA1 (37 kDa), FLA2 (34 kDa) AND FLA3 (32 kDa).
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagellum; Periplasmic.
FT UNSURE 2
FT UNSURE 8
FT UNSURE 9

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FT NON TER          9          9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match      24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
Db 2 TVP 4

RESULT 10
OXYA_SCYCA
ID OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
NCBI_TaxID=7830;
RN [1]
RP SEQUENCE
RC TISSUE=Pituitary; PubMed=7972045;
RX Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RA "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match      24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSV 3
Db 6 CPV 8

RESULT 11
OXYF_SCYCA
ID OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary; PubMed=7972045;
RX Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RA "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match      24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSV 3
Db 6 CPV 8

RESULT 12
OXYT_BUPRE
ID OXYT_BUPRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seritocin (Iser5,Ile8]-oxytocin).
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Bufonidae; Bufo.
NCBI_TaxID=8390;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophysial peptide, seritocin (Iser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: Devoid of oxytocic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 983 MW; 17FF476E5A6D04B CRC64;

Query Match      24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVPL 5
Db 5 SCPI 8

RESULT 13
OXYV_SQUAC
ID OXYV_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;

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RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match      24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSV 3
Db 6 CPV 8

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